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OM nucleic - nucleic search, using sw model

Run on: July 7, 2003, 03:15:26 : Search time 101 Seconds
 (without alignments)
 5902.769 Million cell updates/sec

Title: US-10-086-464-1
 Perfect score: 1944
 Sequence: 1 atgtctccaggcgctctcc.....atagtggacctctctttaa 1944

Scoring table: IDENTITY_NDC
 Gapop 10.0 , Gapext 1.0

Searched: 44362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : Issued Patents.NA.*
 1: /cgn2.6/ptodata/1/ina/5A.COMB.seq.*
 2: /cgn2.6/ptodata/1/ina/5B.COMB.seq.*
 3: /cgn2.6/ptodata/1/ina/6A.COMB.seq.*
 4: /cgn2.6/ptodata/1/ina/6B.COMB.seq.*
 5: /cgn2.6/ptodata/1/ina/PCITUS.COMB.seq.*
 6: /cgn2.6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|-------------------|
| 1 | 152 | 9.4 | 2868 | 4 | US-09-228-986-4 |
| 2 | 178.4 | 9.2 | 3239 | 4 | US-09-228-986-9 |
| 3 | 174.6 | 9.0 | 2432 | 4 | US-09-228-986-7 |
| 4 | 166.4 | 8.6 | 2749 | 1 | US-08-265-628-1 |
| 5 | 162.4 | 8.4 | 4304 | 4 | US-08-881-708-1 |
| 6 | 146.6 | 7.5 | 2571 | 1 | US-07-717-331F-9 |
| 7 | 146.6 | 7.5 | 2833 | 1 | US-07-717-331F-9 |
| 8 | 140.6 | 7.2 | 1554 | 2 | US-08-587-680A-24 |
| 9 | 139.8 | 7.2 | 2749 | 1 | US-07-717-331F-4 |
| 10 | 138.2 | 7.1 | 2389 | 4 | US-09-228-986-1 |
| 11 | 130.8 | 6.7 | 2336 | 4 | US-09-228-986-10 |
| 12 | 121.2 | 6.2 | 966 | 1 | US-08-447-185-2 |
| 13 | 121.2 | 6.2 | 2443 | 1 | US-08-447-185-3 |
| 14 | 117.8 | 6.1 | 3097 | 4 | US-09-228-986-11 |
| 15 | 117.8 | 6.1 | 16442 | 3 | US-08-781-891-208 |
| 16 | 115.2 | 5.9 | 1926 | 4 | US-09-249-585A-2 |
| 17 | 115.2 | 5.9 | 2580 | 3 | US-09-050-863-2 |
| 18 | 115.2 | 5.9 | 2580 | 4 | US-09-359-081-2 |
| 19 | 115.2 | 5.9 | 5452 | 2 | US-09-130-114-1 |
| 20 | 115.2 | 5.9 | 9600 | 4 | US-08-910-647-1 |
| 21 | 115.2 | 5.9 | 9600 | 4 | US-09-620-925-1 |
| 22 | 115.2 | 5.9 | 10596 | 1 | US-07-884-811-15 |
| 23 | 115.2 | 5.9 | 10596 | 1 | US-07-885-971-15 |
| 24 | 115.2 | 5.9 | 10596 | 1 | US-08-087-783A-15 |
| 25 | 115.2 | 5.9 | 10596 | 1 | US-08-194-088B-15 |
| 26 | 115.2 | 5.9 | 10596 | 2 | US-08-194-087-15 |
| 27 | 115.2 | 5.9 | 10596 | 5 | PCT-US93-04648-15 |

28 114.4 5.9 2943 4 US-09-503-922-2 Sequence 2, Appli
 29 110.8 5.7 7218 1 US-08-232-463-14 Sequence 14, Appli
 30 107.6 5.5 51259 3 US-08-781-891-209 Sequence 269, App
 31 101.2 5.2 5733 2 US-08-473-553A-1 Sequence 1, Appli
 32 100.2 5.2 1505 1 US-07-915-246-1 Sequence 1, Appli
 33 98.8 5.1 2649 4 US-09-238-986-12 Sequence 12, Appli
 34 98.2 5.1 913 1 US-08-217-327-3 Sequence 3, Appli
 35 98.2 5.1 913 1 US-07-385-970A-3 Sequence 3, Appli
 36 98.2 5.1 913 1 US-08-238-687A-3 Sequence 3, Appli
 37 98.2 5.1 913 1 US-08-530-797-2 Sequence 3, Appli
 38 98.2 5.1 913 1 US-08-298-829-3 Sequence 3, Appli
 39 98.2 5.1 913 2 US-08-787-335-2 Sequence 2, Appli
 40 96.6 5.0 1984 1 US-07-885-970A-25 Sequence 25, Appli
 41 96.6 5.0 1985 1 US-08-298-829-25 Sequence 25, Appli
 42 96.6 5.0 3489 2 US-08-728-323A-1 Sequence 1, Appli
 43 96.6 5.0 3489 4 US-09-298-568-1 Sequence 1, Appli
 44 96.6 5.0 32207 2 US-08-770-379-20 Sequence 20, Appli
 45 96.6 5.0 32207 2 US-08-770-379-20 Sequence 20, Appli

ALIGNMENTS

RESULT 1
 US-09-228-986-4
 ; Sequence 4, Application US/09228986
 ; Patent No. 6359198

GENERAL INFORMATION:

APPLICANT: Strabala, Timothy

APPLICANT: Nieuwenhuizen, Niels

TITLE OF INVENTION: Compositions Isolated from Plant Cells

TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signalling

FILE REFERENCE: 11000/1020

CURRENT APPLICATION NUMBER: US/09/228.986

CURRENT FILING DATE: 1999-01-12

NUMBER OF SEQ ID NOS: 130

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 4

LENGTH: 2868

TYPE: DNA

ORGANISM: Pinus radiata

US-09-228-986-4

Query Match 9.4%; Score 182; DB 4; Length 2868;
 Best Local Similarity 52.9%; Pred. No. 8.9e-36;
 Matches 467; Conservative 0; Mismatches 400; Indels 15; Gaps 3;

QY 787 TTCACATACGAGGAGCTAGCTAGAGCCACCAATGGTTTCTCCGAGGCGCACTTGTAGGA 846
 1116 TTCTCATTCGGGAATTACAGGTTGCACATGATGGTTTACCAATAGAACATCTCTGGC 1175
 QY 847 CAAGCGGGTTTCGGTTACGTSCACAAAGGTGTGTGCTAGTGGGAAGAAGTTCCTGTG 906
 1176 AGAGGTGGTTTGGAAAGGTGTACAAAGGCGCGCTTCAGATGTTCTCTGGTGGCTGTA 1235
 QY 907 AACCACTTGAAGTTGGAGTGGTCTAG---GGAGAGAGGAGTTTACGAGGAGTTGAG 963
 1236 AAACGCTCTGAAGGAAGAGCGTACCCGGTGGAGATTGCAGTTTCAACAGAGAGGAG 1295
 QY 964 ATCATCAGCAGAGTTTCCACACAGGCACTGTGGTGTCTTGTGTTATTGCATCCCGGT 1023
 1296 ATGATGAGCATGACATACATAGAACCTCTTCGAGTACGTGGATTCTGCATGACACCC 1355
 QY 1024 GCCAAGATGCTTCTTATGAGTTGTTCCTFANCAACAATCTCGAGCTTCACCTCCAT 1383
 1356 ACTGAACGGGTCTTCTTATCCCTACATGGCAATGGAAGTGTGCTTCATGCTACGA 1415
 QY 1084 GCGGAGGAC-----GGCTACATGGAATGAGGACACCATGAGATGCTCTTGA 1137
 1416 GAGAGGACAAATAGCCACCTTAGATTGGCACTCGAAGCGCATAGCATGGGT 1475
 QY 1238 TCTGCTAAAGGACTTCTTATCTCATGAGATTGCAATCCTAAATCATTCACCGAT 1197

Db 1476 TGTGCAAGAGGCTCTCCCTACTTGCATGATCATGCTGATCTCTAAGATTATTCACCGGAT 1535
QY 1198 ATCAAGGCTTCAACATATGATAGATTCAGCTTGAAGCTAGGTTGIGATTGGT 1257
Db 1536 GTCAAGGCTGCTCAACATCTTACTTGGATGAAGATATGAGGCGATGTTGGGGATTTGGC 1595
QY 1258 CTGCTCAAGATGCTTCTGATACAAACAGGCTATCAACAGCTGTGATGGGAACCTTT 1317
Db 1596 TTGGCAAACTTATGATATAGGACACACATGTTACGAGGCTGTCTGTGGAACTAT 1655
QY 1318 GGTACTTGGCTCCGGAATAGCTGCAAGCGGAAGCTCACGGAGAGTCTGAGCTTTTC 1377
Db 1656 GGCACATACAGCACTGAGTACCTTTCTACTGGAAGCTTTTCGGAAGAGACAGAGCTATT 1715
QY 1378 TCATTGGGCTTGTCTTTGGAGCTCATTTACTGGAGCTGACCGCTGATGCCAAGAT 1437
Db 1716 GGTATGGATCATGTTGCTGGAACTTATACGGACACAGGCAATTTG-----ACCTT 1769
QY 1438 GTCTATGTAGACAGCTTATGCTGGGACAGCACTTGTCTTAACGAGCATCTGAG 1497
Db 1770 GCAGCTTTAGCAATGATGATGATGTCATGTTGCTGACCTGAGTTAAAGGCTTACTATAA 1829
QY 1498 CAGGAGACTTTCAGGCTTATGCTGATGCAAGATGATGATGATGATGATGATGATGAT 1557
Db 1830 GAGAGAGGCTTATGATGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1889
QY 1558 ATGGCTCGCATGCTTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1617
Db 1890 GTGGACACTTATCAAGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1949
QY 1618 CGCATGAGCAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1659
Db 1950 AAGATGCTGCAAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1991

RESULT 2
US-09-228-986-9
; Sequence 9, Application US/09228986
; Patent No. 6359198
; GENERAL INFORMATION:
; APPLICANT: Strabala, Timothy
; TITLE OF INVENTION: Compositions Isolated from Plant Cells
; TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signalling
; FILE REFERENCE: 11000/1020
; CURRENT APPLICATION NUMBER: US/09/228,986
; CURRENT FILING DATE: 1999-01-12
; NUMBER OF SEQ ID NOS: 130
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 9
; LENGTH: 3239
; TYPE: DNA
; ORGANISM: Eucalyptus grandis
US-09-228-986-9

Query Match 9.2%; Score 178.4; DB 4; Length 3239;
Best Local Similarity 55.3%; Pred. No. 7.4e-35;
Matches 360; Conservative 0; Mismatches 281; Indels 3; Gaps 1;
QY 787 TTCATACAGGAGCTAGCTAGAGCCAAATGTTTCTCCGAGGCACTTGTAGGA 846
Db 2026 TTCTCTATGATGAACCTTAAGAGGCTGCAACCAATATTTCTCCGATGCAATGAATAGGC 2085
QY 847 CAAGCGGGTTCGGTTACGTTSCAAAGGTTGTTGCTAGTGGGAAGAGTTGCTGTG 906
Db 2086 TTCCGAGATACGGAAGGTTGACAGGGAGTTCTTCTGATGCTATATATAGCAATC 2145
QY 907 AAGCAGTTGAAAGTTGGGAGTGGTTCAGGAGAGAGGAGTTTACGCGAGGTTGAGATC 966
Db 2146 AAGAGCTCAGCAGGGGCTGATCCAGGTTGCAACCGAGTTTACAGAGAAATCGAGCTG 2205
QY 967 ATCAGCAGAGTTTACCAACAGCATCTGGTGTCTTCTGTTGATTTGATGCTGCGCGGTC 1026

Db 2206 CTTTCGGGGTTCATCACAAAGATCTTTGTTGGCCTCATAGGATCTCTTTCAGCAAGGA 2265
QY 1027 AAAGATGCTTCTCTATGAGTTTGTCTTCCCTAACAAACATCTCGAGCTTCACCTCCATGGC 1086
Db 2266 GAGCAGATGTTGGTCTATGATATATGCTTAAACGGGAGCTTCAGGGATAGCTTACAGGA 2325
QY 1087 GAGGAGCGGCTTACAATGGAATGGAGCCAGCATTTGAAGATTTGCTTCTTGGATCTGCTAAA 1146
Db 2326 AAATCAGCATTTATCTTTGATTTGAAGAGGAGGCTTCTGTATAGCTTAGGTTTCGCTAGA 2385
QY 1147 GGATTTCTTATCTTCAATGAGATTTCAATCTTAAATCATTTACCGTGTATATCAGGCT 1206
Db 2386 GGATAGCTTATCTTGCAGAACTCGCAATCTCTCAATTTATCCACAGAGATGTCAAGTCC 2445
QY 1207 TCAACATATTTGATAGATTTTCAAGTTTGAAGCTAGGTTGCTGATTTTGGTCTTCTTAAG 1266
Db 2446 ACCAAATCTTGTGGAGCAACATCTGACGCCAAAGTCGGGATTTTCGGTTTGTCCAAA 2505
QY 1267 ATTCCTTCTGATA---CAAACACGATGATATCAACAGCTGTGATGGGAACTTTGGGTAC 1323
Db 2506 CTGTATCGGACAGCGGGAAGGGGACGCTTTTCGACGCAAGTGAAGGACGCTGGGCTAT 2565
QY 1324 TTGCTCGGGAATAGCTGCAAGCGGAAGCTCAGGGAAGTCTGACGTTTCTTCATTT 1383
Db 2566 TTGATCCGATATCATCATGATCAACAGCTGACAGAAAGAGGATGTGTACAGCTTC 2625
QY 1384 GCGCTTGTGCTTTTGGAGCTCATTTACTGAGCTGACGCTGACCCGTTGA 1427
Db 2626 GGGTGTGCTGCTTTGAGCTCATCTCAACAGCAACGATTTGA 2669

RESULT 3
US-09-228-986-7
; Sequence 7, Application US/09228986
; Patent No. 6359198
; GENERAL INFORMATION:
; APPLICANT: Strabala, Timothy
; TITLE OF INVENTION: Compositions Isolated from Plant Cells
; TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signalling
; FILE REFERENCE: 11000/1020
; CURRENT APPLICATION NUMBER: US/09/228,986
; CURRENT FILING DATE: 1999-01-12
; NUMBER OF SEQ ID NOS: 130
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 2432
; TYPE: DNA
; ORGANISM: Pinus radiata
US-09-228-986-7

Query Match 9.0%; Score 174.6; DB 4; Length 2432;
Best Local Similarity 56.5%; Pred. No. 5.7e-34;
Matches 368; Conservative 0; Mismatches 274; Indels 9; Gaps 2;
QY 787 TTCATACAGGAGCTAGCTAGAGCCAAATGTTTCTCCGAGGCACTTGTAGGA 846
Db 1070 TTCTCTATGATGAACCTTAAGAGGTTTCTTCCACTAATATTTAGTAGCAAGATATTTAGGA 1125
QY 847 CAAGCGGGTTCGGTTACGTTSCAAAGGTTGTTGCTAGTGGGAAAGAGTTGCTGTG 906
Db 1130 GTAGGAGGATATGGAATTTGCTATTAAGGATTTCTTACAGATGSGCACTATAGTACCAATA 1189
QY 907 AAGCAGTTGAAAGTTGGGAGT---GGTCAAGGAGAGGAGGAGTTTTCAGGAGAGGTTGAG 963
Db 1190 AAAAGTTTGAAGATGTTAATGTGGGAGGAGAGAAATCAATTTCAACAGAGGTTGAA 1243
QY 964 ATCATCAGCAGGTTTCAACAGGATCTGGTGTCTCTTGTGTTGTTTATTCATCCCGCT 1023
Db 1250 AIGATCAGCTTGGCTGTGATAGGAACCTTATACGATTTGATGATTTTGGATTTTGCACACCTCC 1309
QY 1024 GCCAAAGATTTGCTTGTATGATGTTTCTTCTTACCAACAATCTCG-----AGCTTCA 1077

Db 1310 ACAGAGAGGCTTCTGCTATACCTACATGCCAATGGAAGTGTGCGCTTCTCTAGA 1369
QY 1078 CTCCTATGGAGGCGGCTACATGGAATGGAATGAGAGCAGATTTGAAGATTGCTCTTGA 1137
Db 1370 GATCATATTAATGGAAGCTTGCCCTGACTGCGCTACTCGCAAGCGTATAGCCCTGGA 1429
QY 1138 TCTGCTAAGAGCTTCTTCTATCTCTATGAGAGTTCGAATGCTTAAATCAATCACCCTGAT 1197
Db 1430 GCAGCTAGGGAGCTGTATATTTGATGAGCAATGTATCCCAAGATTATACCCGGAT 1489
QY 1198 ATCAAGGCTCAACATATTTATGATATTTCAAGTTTGAAGCTTCTGATTTTGGT 1257
Db 149C GTGAAGAGCAAAATATTTACTGGATGATATTTTGAAGCTTCTTGGAGATTGGG 1549
QY 1258 CTCTCTAAGATTCTTCTGATCAAAACAGCGATGTATCAACAGCTGTGTGGAACCTTT 1317
Db 155C TTAGCAAGAGCTTTGATCACAGGATTTCTCATGTGACTACTGCTGTCGAGGAGGTA 1609
QY 1318 GGTACTTGGCTCCGAATACCTGCAAGCGGAAGCTCAGCGAGAAGTCTGACGTTTC 1377
Db 151C GGTACATTTGCCCAAGATACCTTTCAACGGGACAATCTTCAGAGAAAATGATGATTT 1669
QY 1378 TCAATTTGGCTGTGCTTTTGGAGCTTACTTACGAGCTGACCGCTTGAT 1428
Db 1670 GGCCTGGATATTTACTGTTGGAATCATTACAGGACAGAGGCTTTAGAT 1720

RESULT 4

US-08-265-628-1
; Sequence 1, Application US/08265628
; Patent No. 5821094
; GENERAL INFORMATION:
; APPLICANT: Rothstein, Steven J.
; APPLICANT: Goring, Daphne
; TITLE OF INVENTION: S-LOCUS RECEPTOR KINASE GENE IN A
; TITLE OF INVENTION: SELF-INCOMPATIBLE BRASSICA NAPUS LINE
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 W. Madison St. Suite 3400
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60661

COMPUTER READABLE FORM: disk
MEDIUM TYPE: Floppy
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
FILING DATE: US/08/265,628
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/959,945
FILING DATE: US/07/847,564
APPLICATION NUMBER: US/07/847,564
FILING DATE: 03-MAR-1992

ATTORNEY/AGENT INFORMATION:
NAME: Pochopien Ph.D., Donald J.
REGISTRATION NUMBER: 32,167
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-707-8889
TELEFAX: 312-707-9155

INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2749 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO

ORIGINAL SOURCE:
ORGANISM: Brassica napus
STRAIN: oleifera
INDIVIDUAL ISOLATE: W1
POSITION IN GENOME:
CHROMOSOME/SEGMENT: S-locus
FEATURE:
NAME/KEY: CDS
LOCATION: 1..2574
PUBLICATION INFORMATION:
AUTHORS: GORING, DAPHNE
AUTHORS: ROTHSTEIN, STEVEN J.
TITLE: THE S-LOCUS RECEPTOR KINASE GENE IN A
TITLE: SELF-INCOMPATIBLE BRASSICA NAPUS LINE ENCODES A
TITLE: FUNCTIONAL SERINE/THREONINE KINASE
RELEVANT RESIDUES IN SEQ ID NO: 1: FROM 1 TO 2749
US-08-265-628-1

Query Match 8.68; Score 166.4; DB 1; Length 2749;
Best Local Similarity 56.44; Pred. No. 6.6e-32;
Matches 352; Conservative 0; Mismatches 266; Indels 5; Gaps 2;

QY 796 GAGGAGCTAGTAGAGCCACCAATGGTTCTCCGAGGCGGAACCTTGTAGGACAAAGCGCGG 855
Db 1558 GAAGCTGTTGTCAAGGCCACCGGAAATTTCTCCAAATTTGTAACAACCTCGGACAAAGTGGT 1617
QY 856 TTGCGTTACGTGCACAAAGGTGTTGCTAGTGGGAAGAGTGTCTGCGAAGCAGTTG 915
Db 1618 TTGCGTTATGTTTACAAAGGTAGATTACTTGTATGGCAAGAAATTTGCCGTAAAAAGGCTA 1677
QY 916 AAGTTGGAGTGTGTCAGGAGAGAGGAGTTCAGGCAGAGGTTGAGATCATCAGCAGA 975
Db 1678 TCAAAAAGTGGCTCAAGGAGCTGGTGAGTTATGATGAGGTGAGATTGATCGCGAGG 1737
QY 976 GTTCACCAAGGCTATGCTGCTCTCTGTTGGTTATGATCGCGGTGCCAAAGATTG 1035
Db 1738 CTTGAGCATATAAACCCTTGCCGATTTCTTGGCTTGCTGATGAGGACAGCAGAAAGTG 1797
QY 1036 CTTGCTATGAGTTTGTCTTAAACAACATCTCAGCTTCCCTCCATGG---CGAGGA 1092
Db 1798 CTGTAATAGTATTTAGAAAATTTAAGCCTCGATCTTCTCTCGSAAATAAAGCA 1857
QY 1093 CGGCTACATGAATGAGCAGCAGCAGATTTGAAGTTGCTCTGATCTGCTAAGGACTT 1152
Db 2858 AGCTACGTTAAATTTGAAGGACAGATTTCAACATTTGCTGCTGAGGAGGACTT 1917
QY 1153 TCTTATCTTATGAAGATTGCAATCTCTAAATCTTCAATCTCACCCTGATATCAAGGCTTCAAC 1212
Db 1918 TTATATCTTATCAGACTCAGCGTTTAGGATAATCCACAGAGATATGAAAGTAAGTAA 1977
QY 1213 ATATTGATAGATTTCAGTTTGAAGCTTAAGTTGCTGATTTTGGTCTTGTCTAAGATTGCT 1272
Db 1978 ATTTTGTCTGTAIAAAATATGACCAAGAGATCTCGGATTTTGGGATGCCAGAAATCTTT 2037
QY 1273 TCTGATACAAACAGCATGTATCAACAG---TGTGATGGGAACCTTTGGTACTTGTGCT 1329
Db 2038 GCAAGGGACGAGCTGAGCTAAGCTAACAAGGAGGTTGGTCGGAAGTCTAGCGGTACATGCT 2097
QY 1330 CCGGANTACGCTGCAAGCGGAAAGCTCAGCGAGAAGTCTGAGCTTTTCTCAATTTGGCGTT 1389
Db 2098 CCGGAGTACGCAATGATGGGTATTTCTCGGAAAAATCAGATGTTTTCAGTTTGGAGTC 2157
QY 1390 GTGCTTTTGGAGCTCATTTACATGGA 1413
Db 2158 ATTGTTCTTGAATTTGTTAGTGA 2181

RESULT 5

US-08-881-706-1
; Sequence 1, Application US/08881706
; Patent No. 6245969
; GENERAL INFORMATION:
; APPLICANT: Chong, Joase

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; APPLICANT: Li, Jianming
; TITLE OF INVENTION: Receptor Kinase BIN1
; FILE REFERENCE: 07251/022001
; CURRENT APPLICATION NUMBER: US/08/881,706
; CURRENT FILING DATE: 1997-06-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 4104
; TYPE: DNA
; ORGANISM: Arabidopsis sp.
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (97)...(3687)
US-08-881-706-1

Query Match      8.4%; Score 162.4; DB 4; Length 4104;
Best Local Similarity 55.4%; Pred. No. 7.9e-31;
Matches 382; Conservative 0; Mismatches 296; Indels 12; Gaps 3;

QY 788 TCACATACGAGGAGCTAGCTAGAGCCACCAATGGTTTCCCGAGGCGAATCTGTAGGAC 847
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
; 2708 TCACGTTCCGATCTCTCTAGGCTACCAATGGTTTCCATATGATGATGCTGATGGTT 2767
QY 848 AAGCGGGTTCGTTACGTGCAAAAGGTGTGTGCCIAGTGGGAAAGAGTTGCTGTGA 907
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
; 2768 CTGGTGGTTTGGAGATGTTTACAAAGCGATTTGAAAGATGGAAGCGGCTGGCTATCA 2827
QY 908 AGCAGTTTAAAGTTGGAGTGTCTAGGAGAGGAGGTTTTCAGGAGAGGTTGATGATCA 967
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
; 2828 AGAAATGATTCATGTTAGCGGTCAAGGTGATAGAGATTCATGGCGGAGATGGAACCA 2887
QY 968 TCAGCAGATTCACACAGCATCTGCTGCTCTCTGTTGTTATTCATCGCGGGTGCCA 1027
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
; 2888 TTGGGAAGATCAACATCAAAATCTGTGCCCTCTCTGTTGTTATTCGAAAGTTGGAACG 2947
QY 1028 AAGATGTTGTTCTATGATGTTTGTCTTCAACAAATCTCGAGCTTCACCTCCATGGC- 1086
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
; 2948 ACCGGCTCTCTGTTAATGAGTTATGAACTATGGAAGTTAGAGATGTTTGCAGAGCC 3007
QY 1087 -----GAGGAGGCGCTCAATGGAATGAGGAGCACCAGATGGAAGATTCCTTGGATCG 1141
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
; 3008 CCAAGAAAGGTGGGTGAAACTTAAATTTCCACACGCGGGAAGATTCGATAGGATCAG 3067
QY 1142 CTAAAGAGCTTCTTATCTTCATGAGATGCAATCTCAATCTTAAATCATTCACCGTATCA 1201
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
; 3068 CTAGAGGCTGCTCTCTCTTCCACACACTGCGATCCGATATCATCCACAGAGATGA 3127
QY 1202 AGGCTTCAACATATGATAGATTTCAAGTTTGAAGTGAAGTTCGTTGTTGTTGTTG 1261
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
; 3128 AATCCAGTAAATGTTGTTGATGAGAATTTGGAAGCTCGGTTTCAGATTTTGGCATGG 3187
QY 1262 CTAAGNTGCTTCTGATACAAACAGCATGATACACAGT---GTGATGGGAACCTTTG 1318
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
; 3188 CGAGGCTGATGATGCGATGCGATGCAATTTAAGCGTCACTAGTATGCTGTACACCGG 3247
QY 1319 GGTATGCTGCTCGGAATACGCTGCAAGCGGAAAGCTCACGAGAGATCTGACGTTTCT 1378
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
; 3248 GTTAGTCTCTCCAGATTTACCAAGTTTCAGTGTTCACAAAGAGAGAGCTTTATA 3307
QY 1379 CATTTGGGGTGTGCTTTTGGAGCTCATTTACTGAGAGTCTGACCCGCTTGTATGCCAATG 1438
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
; 3308 GTTACGGTGTGCTCTACTCGAGCTACTCAGCGTAAACGGCCACAGGATTCACCGGAT- 3366
QY 1439 TCTATGTAGATGACAGCTTAGTTGACTGGG 1468
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
; 3367 --TTTGGAGATACCAACCTTGTGGATGGG 3394

RESULT 6
US-07-717-331F-9
; Sequence 9, Application US/07717331F
; Patent No. 5484905
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; GENERAL INFORMATION:
; APPLICANT: June Nasrallah; Michael Nasrallah; and Joshua
; APPLICANT: Stein
; TITLE OF INVENTION: A Receptor Protein Kinase Gene
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Yahwak & Associates
; STREET: 25 Skytop Drive
; CITY: Trumbull
; STATE: Connecticut
; COUNTRY: USA
; ZIP: 06611
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: Macintosh
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Microsoft Word
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/17,331F
; FILING DATE: June 19th 1991
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: George M. Yahwak
; REGISTRATION NUMBER: 26,824
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (203)268-1951
; TELEFAX: (203)268-1951
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2571 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-07-717-331F-9
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Query Match      7.5%; Score 145.6; DB 1; Length 2571;
Best Local Similarity 54.6%; Pred. No. 5.4e-27;
Matches 337; Conservative 0; Mismatches 274; Indels 6; Gaps 2;

QY 803 TAGCTAGAGCCACCAATGTTTCTCCGAGCGCACTGTTAGGACAAAGCGGTTCCGTT 862
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
; 1562 TTCTCAAGCCACCGAAATTTCTCCAGCTGTACAAACTCGGACAAAGTGGTTTGGTA 1621
QY 863 ACCTGCACAAAGGTGTGTTGCCCTAGTGGGAAAGATTTGCTGTGAAGCAGTTGAAAGTTG 922
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
; 1622 TTCTTACAGGGAAGATTTACTTTCAGCGGAAAGAAATTCAGTAAAGGCTATCAAGA 1681
QY 923 GGAGTGTTCAGGAGAGAGGAGTTTCAGCAGAGGTTGAGATCATCAGCAGAGTTCCACC 982
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
; 1682 CGTCAGTTCAAGGACTGATGATTTATGAAATGAGGTGACACTAATTCGAGCTTCAGC 1741
QY 983 ACAGGATCTGTTGTTCTCTTGTGTTGTTATTCATCGCGGTGCAAAAGATTTGCTTGTCT 1042
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
; 1742 ATATAACCTTGTTCAGTTCTTGGCTGTTCATTTGAAGGAGATGAGAAGATGTGATAT 1801
QY 1043 ATGAGTTGTTCTTACACAAATCTCAGCTTCACCTCCATGGGA---GGGAGGCGCTA 1099
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
; 1802 ATGAGTATTTGGAAAAATTTAAGCCTTGATCTTCTTCTTTGTTAAACCCGAGGTCTA 1861
QY 1100 CAATGAATGGAGCACCAGATTTGAAGATGCTCTTGGATCTGCTAAAGGACTTCTTATC 1159
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
; 1862 AGCTAAATTTGGAATGAGATTCGACATTTACCAATGGTGTGTTCTCGAGGCTTTTATC 1921
QY 1160 TTCAIGAAGATTGCAATCTTAAATCATTCACCGTATATCAAGGCTTCAACATATTA 1219
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
; 1922 TTCAICAGACTCACCGTTTAGGATAATCCACAGAGATTTGAAAGTAAGTAACATTTTC 1981
QY 1220 TAGATTTCAAGTTTGAAGCTAAGGTTGCTGATTTTGGTCTTGTCTAAGA---TTGCTTCTG 1276
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
; 1982 TTGACAAAAATATGATCCCAAGAGATCTCGGATTTTGGGATGGCCAGGATATTTGAAGGG 2041
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QY 1277 ATACAAACGCGCATGTATCAACACGCTGTGTGATGGAACTTTGGTACTTGGTCTCCCGAAT 1336
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Db 2042 ACGAAC3GAACTACACAACTAAGGTGTCGGAACATACGCTACATGTCCCGGAAT 2101
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1337 ACCTCTCAAGCGGAAAGCTCACGGAAG*CTGACGTTTCTCATHTGGGCTGTGCTTT 1396
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Db 2102 ACCTCAATGTATGGATATCTCGGAAATCATGATGTTTCAGTTTGGAGTCATAGTC 2161
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1397 TGGAGCTCATTACTGGA 1413
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2162 TTGAATTTGTAGTGA 2178
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 7
US-07-717-331F-1
; Sequence 1, Application US/07717331F
; Patent No. 5484905
; GENERAL INFORMATION:
; APPLICANT: June Nasrallah; Michael Nasrallah; and Joshua
; APPLICANT: Stein
; TITLE OF INVENTION: A Receptor Protein Kinase Gene
; TITLE OF INVENTION: Encoded At The Self-Incompatibility Locus
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Yahwak & Associates
; STREET: 25 Skytop Drive
; CITY: Trumbull
; STATE: Connecticut
; COUNTRY: USA
; ZIP: 06611
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: Macintosh
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Microsoft Word
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07717,331F
; FILING DATE: June 19th 1991
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: George M. Yahwak
; REGISTRATION NUMBER: 26,824
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (203)268-1951
; TELEFAX: (203)268-1951
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2833 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-07-717-331F-1

Query Match: 7.5%; Score 146.6; DB 1; Length 2833;
Best local similarity 54.6%; Pred. No. 5.6e-27;
Matches 337; Conservative 0; Mismatches 274; Indels 6; Gaps 2;

QY 803 TAGCTAGACCCACCAATGGTTTCTCGAGCGCACTGTAGGACAAAGCGGGTTCGGTT 862
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1562 TTGTCAAGCCACCGGAAATTTCTCCAGCTGTACAAACCTCGGACAAAGTGGTTTGGA 1621
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 863 ACCTGCACAAAGGISTGTTCCTAGTGGGAAAGTGTCTGTGAAGCACTTGAAGTTG 922
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1622 TTGTTTACAGGGAAGATTAATCTACGGGAAAGAAATTCAGTAAAGGCTATCAAGA 1681
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 923 GGAGTGGTCAGGAGAGAGAGGAGTTTCAGGACAGAGTTGAGATCATCAGCAGAGTTCACC 982
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1682 CGTCAGTTCAAGGACTGA-TGATTTATGATGAGGTGACACTAATTCGAGGCTTCAGC 1741
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 983 ACAGGCATCTGGTGTCTCTGTGGTGTATGTCATCCCGGTGCGCAAGATTCCTGTCT 1042
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1742 ATATAAACCTTGTTCAGS-TCTTGGCTGTTCATTTGAAGGAGATGAGAAGTGTGATAT 1801
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

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QY 1043 ATGASITGTTCCTAACAAACAAATCTCGAGCTTCACCTCCATGGCGA---GGACGGCTTA 1099
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Db 1802 ATGAGTATTTGGAATTTAAAGCTTTGATTTCTATCTCTTTGTAATAACCCGAGGTCTTA 1861
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1100 CAATGGGAATGAGCAGACAGATTGAAGATTGCTCTTGGATCTGCTAAAGGACATTTCTTATC 1159
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Db 1862 AGCTAATTTGAANTGAGAGATTCGACATTTACCAATGGTGTGCTCGAGGGCTTTTATATC 1921
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1160 TTCTAGAGATTGCAACCTAAATCATTCACCGTGATACAGGCTTCAACACATATGA 1219
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Db 1922 TTCATCAAGACTCACGGTTTAGGATAATCCACAGAGATTGGAAGTAAGTAACATTTTGC 1981
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1220 TAGATTTCAAGTTTCAGCTAAGCTTGTCTGATTTGTTGTTCTTCTAAGA---TTGCTTCTG 1276
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Db 1982 TTGACAAAATATGATCCCAAGATCTCGGATTTTGGATGGCCAGGATATTTGAAAGG 2041
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QY 1277 ATACAAACACGCATGTATCAACACGCTGTGATGGGAACCTTTGGGTACTTGGCTCGGAAT 1336
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Db 2042 ACGAAACGGAAGCTAACACAATGAAGTGTGTCGGAACATACGGCTACATGTCCCGGAAT 2101
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1337 ACGTGAAGCGGAAAGCTCACGGAAGTCTGAGAGAGTCTGACGTTTCTCATHTGGGCTGTGCTTT 1396
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Db 2102 ACCTCAATGTATGGATATCTCGGAAATCATGATGTTTCAGTTTGGAGTCATAGTC 2161
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QY 1397 TGGAGCTCATTACTGGA 1413
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2162 TTGAATTTGTAGTGA 2178
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 8
US-08-587-680A-24
; Sequence 24, Application US/08587680A
; Patent No. 5977434
; GENERAL INFORMATION:
; APPLICANT: Ronald, Pamela C.
; APPLICANT: Wang, Guo-Liang
; APPLICANT: Song, Wen-Yuang
; APPLICANT: Szabo, Veronique
; TITLE OF INVENTION: Procedures and Materials for Conferring
; TITLE OF INVENTION: Disease Resistance in Plants
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/587,680A
; FILING DATE: 17-JAN-1996
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/475,891
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: US 60/004,645
; FILING DATE: 29-SEP-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/567,375
; FILING DATE: 04-DEC-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Bastian, Kevin L.
; REGISTRATION NUMBER: 34,774

```


RESULT 10

US-09-228-986-1

; Sequence 1, Application US/09228986

; Patent No. 6359198

; GENERAL INFORMATION:

; APPLICANT: Strabala, Timothy

; APPLICANT: Nieuwenhuizen, Niels

; TITLE OF INVENTION: Compositions Isolated from Plant Cells

; TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signalling

; FILE REFERENCE: 11000/1020

; CURRENT APPLICATION NUMBER: US/09/228,986

; CURRENT FILING DATE: 1999-01-12

; NUMBER OF SEQ ID NOS: 130

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 1

; LENGTH: 2389

; TYPE: DNA

; ORGANISM: Pinus radiata

US-09-228-986-1

Query Match

; Sequence 1, Application US/09228986

; Patent No. 6359198

; GENERAL INFORMATION:

; APPLICANT: Strabala, Timothy

; APPLICANT: Nieuwenhuizen, Niels

; TITLE OF INVENTION: Compositions Isolated from Plant Cells

; TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signalling

; FILE REFERENCE: 11000/1020

; CURRENT APPLICATION NUMBER: US/09/228,986

; CURRENT FILING DATE: 1999-01-12

; NUMBER OF SEQ ID NOS: 130

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 1

; LENGTH: 2389

; TYPE: DNA

; ORGANISM: Pinus radiata

US-09-228-986-1

Query Match

; Sequence 1, Application US/09228986

; Patent No. 6359198

; GENERAL INFORMATION:

; APPLICANT: Strabala, Timothy

; APPLICANT: Nieuwenhuizen, Niels

; TITLE OF INVENTION: Compositions Isolated from Plant Cells

; TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signalling

; FILE REFERENCE: 11000/1020

; CURRENT APPLICATION NUMBER: US/09/228,986

; CURRENT FILING DATE: 1999-01-12

; NUMBER OF SEQ ID NOS: 130

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 1

; LENGTH: 2389

; TYPE: DNA

; ORGANISM: Pinus radiata

US-09-228-986-1

Query Match

; Sequence 1, Application US/09228986

; Patent No. 6359198

; GENERAL INFORMATION:

; APPLICANT: Strabala, Timothy

; APPLICANT: Nieuwenhuizen, Niels

; TITLE OF INVENTION: Compositions Isolated from Plant Cells

; TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signalling

; FILE REFERENCE: 11000/1020

; CURRENT APPLICATION NUMBER: US/09/228,986

; CURRENT FILING DATE: 1999-01-12

; NUMBER OF SEQ ID NOS: 130

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 1

; LENGTH: 2389

; TYPE: DNA

; ORGANISM: Pinus radiata

US-09-228-986-1

QY 1539 TCGTATGACAGAGAGAGATGGCTCCATGGTGTGCTCGCGGTGTGTTCCGCA 1598
Db 1894 CAAAAACATTGAAGAGAGAACTAGTAGCTTTCAGATTTCCTGCTGCTCACA 1953
QY 1599 TCGAGTCGCGCAGACACTCGCATGAGCAGATGTGCGTGGTTCAGAGAAAT 1653
Db 1954 AICTCTCAGCAACGCCCTAAATGAGCCATGCTGAGGGTGAITCAAGACATT 2008

RESULT 11

US-09-228-986-10

; Sequence 10, Application US/09228986

; Patent No. 6359198

; GENERAL INFORMATION:

; APPLICANT: Strabala, Timothy

; APPLICANT: Nieuwenhuizen, Niels

; TITLE OF INVENTION: Compositions Isolated from Plant Cells

; TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signalling

; FILE REFERENCE: 11000/1020

; CURRENT APPLICATION NUMBER: US/09/228,986

; CURRENT FILING DATE: 1999-01-12

; NUMBER OF SEQ ID NOS: 130

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 10

; LENGTH: 2336

; TYPE: DNA

; ORGANISM: Pinus radiata

US-09-228-986-10

Query Match 6.7%; Score 130.8; DB 4; Length 2336;
Best Local Similarity 50.4%; Pred. No. 4.4e-23;
Matches 346; Conservative 0; Mismatches 33; Indels 3; Gaps 1;

QY 787 TTACATACGACGAGCAGTAGCTAGAGCCACCAATGGTTTCTCCGAGGCGAACTTTAGGA 846
Db 1024 TTCGATTACAGGAGCTGGGTATCCGCCGCGAGGGTTTCGCGACGAAACCTTTGGGG 1083
QY 847 CAAAGCGGGTTCGTTACGTGCAACAAAGGTGTTCCTAGT---GGGAAAGAGTTGCT 903
Db 1084 TAGCGGGGATTTGGCATGGTTTACAAGGGTTTCTCCCCAGAGCGGCCCAAGAAGTCGA 1143
QY 904 GTGAACAGCTTGAAGTTGGGAGTGTCCAGGAGAGAGGAGCTTCAGGACGAGGTTGAG 963
Db 1144 GTGAATGTATACGAGGAGTTCAGGAGGAGTTCAGGAGGAGTTCAGGAGGAGTTCGA 1203
QY 964 ATCATCAGCAGAGTTTCCACACAGGCACTGGTGTCTTTTGGTTTATTCATCGCGGT 1023
Db 1204 AGCATGGGCGGCTACAGCAGCCGAACTGGTTCAACTCCGAGGAGTTCGCGAAGGCAT 1263
QY 1024 GCCAAAGAGTTGCTTGTCTATGAGTTTGTCTTAACAACAATCTCAGCTTCACTCCAT 1083
Db 1264 ACACAGCTATTTCATCGTTTACGACTACATGCCCAAGGAGGCTGCATAAATCATCTTC 1323
QY 1084 GCGAGGGAGCGCTTACATGGAATGGAGCACCAGATTTGAAGATTGCTCTTGGATCTGCT 1143
Db 1324 GGTAGTCCGACAAACAGTCTCTGCGGATCGCGATACGCGATCTCCTAAAGGCGGTAGCA 1383
QY 1144 AAAGGAGCTTCTTATCTTCTCATGAAGATTGCAATCTCTAAATCATTCACCGTGATATCAAG 1203
Db 1384 GCGGGGCTGCTGTATCTGTACAGCAGCAATGGGAGAGAGGGTCTGCCACAGGAGCATTAAG 1443
QY 1204 GCTTCAACAGATTTGATAGATTTCAGTTTGAAGCTAAGCTAGCTGCTGATTTGGTCTGCT 1263
Db 1444 TCAGCAACAGCTGCTGTGTGATTTCGAGTTTCAACGGGCGCTTAGTACATTCGCGCTCGCT 1503
QY 1264 AAGATTGCTCTGTATACAAACAGCATGTATCAACAGCTGTGATGGGAGAGCTTTGGGTAC 1323
Db 1504 CGGCTGTATGATCAGATGAGATTCGAGAGAGCAGATATGTGTGAGGAGCTTTGGGTAC 1563
QY 1324 TTGGTCCGGAATACGCTGCAAGCGGAAAGCTCAGGAGAGTCTCAGCTTTTCTCATTT 1383
Db 1564 ATAGCAGCGAGTTTGTATACAAACGAGGAGGAGCACTCTAGCTCGGACCGCTTCAGCTTC 1623


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RESULT 14
US-09-228-986-11
; Sequence 11, Application US/09228986
; Patent No. 6359193
; GENERAL INFORMATION:
; APPLICANT: Strabala, Timothy
; APPLICANT: Nieuwenhuizen, Niels
; TITLE OF INVENTION: Compositions Isolated from Plant Cells
; TITLE OF INVENTION: and Their Use in the Modification of Plant Cells
; FILE REFERENCE: 11000/1020
; CURRENT APPLICATION NUMBER: US/09/228,986
; CURRENT FILING DATE: 1999-01-12
; NUMBER OF SEQ ID NOS: 130
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 11
; LENGTH: 3097
; TYPE: DNA

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RESULT 15
US-08-781-891-208
; Sequence 208, Application US/08781891
; Patent No. 6090520
; GENERAL INFORMATION:
; APPLICANT: Fu, Ying-Hui
; APPLICANT: Yu, Chang-En
; APPLICANT: Oshima, Junko
; APPLICANT: Mulligan, John T.
; APPLICANT: Schellenberg, Gerald D.
; TITLE OF INVENTION: GENE AND GENE PRODUCTS RELATED TO
; TITLE OF INVENTION: WERNER'S SYNDROME
; NUMBER OF SEQUENCES: 209
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED AND BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle

```


GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 7, 2003, 07:27:14 ; Search time 5106 Seconds
(without alignments)
11080.269 Million cell updates/sec

Title: US-10-086-464-1
Perfect score: 1944
Sequence: 1 atgtctctggcgccgtctcc.....atagtgcattctcttttaa 1944

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues
Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 20000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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- 2: gb_hgt.*
- 3: gb_in.*
- 4: gb_cm.*
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- 32: em_hgt_other.*
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- 35: em_hgt_rtd.*
- 36: em_hgt_mam.*
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- 38: em_sy.*
- 39: em_hgt_hum.*
- 40: em_hgt_mus.*
- 41: em_hgt_other.*

Pred. Nc. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match % | Length | DB | ID | Description |
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| 1 | 1944 | 100.0 | 1944 | 6 | AX088876 | AX088876 Sequence |
| 2 | 1944 | 100.0 | 2189 | 8 | AY028699 | AY028699 Brassica |
| 3 | 1369.4 | 70.4 | 2098 | 8 | AY128792 | AY128792 Arabidops |
| 4 | 1369.4 | 70.4 | 2116 | 8 | AY056788 | AY056788 Arabidops |
| 5 | 1369.4 | 70.4 | 2188 | 8 | AY059901 | AY059901 Arabidops |
| 6 | 1369.4 | 70.4 | 2190 | 8 | AY093065 | AY093065 Arabidops |
| 7 | 1367.8 | 70.4 | 2257 | 8 | AF370509 | AF370509 Arabidops |
| 8 | 1341.2 | 69.0 | 2324 | 8 | AY089024 | AY089024 Arabidops |
| 9 | 516.2 | 26.6 | 1902 | 6 | AX088882 | AX088882 Sequence |
| 10 | 516.2 | 26.6 | 1939 | 6 | AX088881 | AX088881 Sequence |
| 11 | 446.6 | 23.0 | 79706 | 8 | AB020746 | AB020746 Arabidops |
| 12 | 427.2 | 22.0 | 2025 | 6 | AX088885 | AX088885 Sequence |
| 13 | 427.2 | 22.0 | 2104 | 6 | AX088884 | AX088884 Sequence |
| 14 | 413.6 | 21.3 | 2196 | 6 | AX088888 | AX088888 Sequence |
| 15 | 413.6 | 21.3 | 2261 | 6 | AX088887 | AX088887 Sequence |
| 16 | 405.8 | 20.9 | 2046 | 8 | AY113039 | AY113039 Arabidops |
| 17 | 405.8 | 20.9 | 2616 | 8 | AF424623 | AF424623 Arabidops |
| 18 | 405.8 | 20.9 | 2735 | 8 | AY075681 | AY075681 Arabidops |
| 19 | 402.8 | 20.7 | 1615 | 8 | AY060577 | AY060577 Arabidops |
| 20 | 399.6 | 20.6 | 2158 | 8 | AY113877 | AY113877 Arabidops |
| 21 | 399.6 | 20.6 | 3064 | 8 | AY035076 | AY035076 Arabidops |
| 22 | 353.2 | 18.2 | 174752 | 8 | AC069324 | AC069324 Oryza sat |
| 23 | 305.6 | 15.7 | 2196 | 6 | AX088879 | AX088879 Sequence |
| 24 | 305.6 | 15.7 | 2231 | 6 | AX088878 | AX088878 Sequence |
| 25 | 301.8 | 15.5 | 53393 | 8 | AF000382 | AF000382 Arabidops |
| 26 | 240.8 | 12.4 | 2062 | 8 | AY096404 | AY096404 Arabidops |
| 27 | 240.8 | 12.4 | 2169 | 8 | AY063963 | AY063963 Arabidops |
| 28 | 229.6 | 11.8 | 75508 | 8 | AB026654 | AB026654 Arabidops |
| 29 | 228.6 | 11.8 | 2837 | 8 | AY058259 | AY058259 Arabidops |
| 30 | 216 | 11.1 | 145120 | 8 | AP003434 | AP003434 Oryza sat |
| 31 | 215.8 | 11.1 | 2414 | 8 | AF106957 | AF106957 Nicotiana |
| 32 | 211.5 | 10.9 | 2266 | 8 | AY133858 | AY133858 Arabidops |
| 33 | 211.5 | 10.9 | 2936 | 8 | AY091071 | AY091071 Arabidops |
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| 35 | 204.6 | 10.5 | 1419 | 8 | AF332429 | AF332429 Arabidops |
| 36 | 204.6 | 10.5 | 1440 | 8 | AY093964 | AY093964 Arabidops |
| 37 | 204.6 | 10.5 | 1754 | 8 | AF367265 | AF367265 Arabidops |
| 38 | 196.6 | 10.1 | 1158 | 8 | AY064968 | AY064968 Arabidops |
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| 41 | 194.8 | 10.0 | 113566 | 8 | AC002330 | AC002330 Arabidops |
| 42 | 194.8 | 10.0 | 194892 | 8 | ATCRRIV6 | ATCRRIV6 Arabidops |
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ALIGNMENTS

RESULT 1
AX088876
LOCUS AX088876
DEFINITION Sequence 1 from Patent WO0114563.
ACCESSION AX088876
VERSION AX088876.1 GI:13397639
KEYWORDS
SOURCE rape.
ORGANISM Brassica napus
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE 1 (bases 1 to 1944)
AUTHORS Goring D. and Silva N.
TITLE Proline-rich extensin-like receptor kinases

AX088876 1944 bp DNA linear PAT 17-MAR-2001

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| QY | 733 | CCAGTTCTCTCCACCGCTCCAGGCTGTGTTAGGCTTCTCCAAAAGCATTTCACA | 792 |
| Db | 854 | CCGGTTCTCTCCACCACTCCAGGCTGTGTTAGGCTTCTCTAAAAGCATTTCACA | 913 |
| QY | 793 | TACGAGGAGTACCTAGACCCACCAATGTTCTCGAGCGCAACTTGTAGCACAGGC | 852 |
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| QY | 853 | GGGTTGGTTAGCTGCACAAAGGTGTGTTGCCCTAGTGGAAAGAGTGTCTGTGAAGCAG | 912 |
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| Db | 1034 | TTGAAGTCTGGTGGTGGTTCAGGAGAGAGAGTTCAGCGTGGAGTTCAGCGTTCAGTTC | 1093 |
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| Db | 1094 | AGAGTTCCACACGAGCCT | 1153 |
| QY | 1033 | TTGCTTGTCTAGTGTCT | 1092 |
| Db | 1154 | TTACTTGTCTAGTGTCT | 1213 |
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| Db | 1214 | CGGCTTCAATGGAATGAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAG | 1273 |
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| DEFINITION | Arabidopsis thaliana clone 17909 mRNA, complete sequence. | | |
| ACCESSION | AY089024 | | |
| VERSION | AY089024.1 | GI:21407798 | |
| KEYWORDS | FLI_CDNA. | | |
| SOURCE | thale cress. | | |
| ORGANISM | Arabidopsis thaliana | | |
| REFERENCE | 1 (bases 1 to 2324) | | |
| AUTHORS | Haas,B.J., Volkovskiy,N., Town,C.D., Troukhan,M., Alexandrov,N., Feldmann,K.A., Flavell,R.B., White,C. and Salzberg,S.L. | | |
| TITLE | Full-length messenger RNA sequences greatly improve genome annotation | | |
| JOURNAL | Genome Biol. (2002) In press | | |
| REFERENCE | 2 (bases 1 to 2324) | | |
| AUTHORS | Brover,V., Troukhan,M., Alexandrov,N., Lu,Y.-P., Flavell,R. and Feldmann,K. | | |
| TITLE | Full-length cDNA from Arabidopsis thaliana | | |
| JOURNAL | Unpublished | | |
| REFERENCE | 3 (bases 1 to 2324) | | |
| AUTHORS | Brover,V., Troukhan,M., Alexandrov,N., Lu,Y.-P., Flavell,R. and Feldmann,K. | | |
| TITLE | Direct Submission | | |
| JOURNAL | Submitted (11-MAR-2002) Ceres, Inc, 3007 Malibu Canyon Road, Malibu, CA 90265, USA | | |
| COMMENT | This clone sequence is one of 5,000 Ceres full-length cDNAs made available to TIGR and Genbank. The following quality assessment of this set was done by comparison with known proteins: two percent of the clones are estimated to be 5'-truncated; less than one percent are 3'-truncated; approximately two percent represent alternative splice variants, including unspliced introns and spliced exons; one percent may contain premature stop codons; five percent may have frame shifts in a coding region. A sequence is considered to be 5'-truncated if it lacks the translation initiation start (ATG). A C-terminal end of the encoded protein. Please note that these cDNA sequences are derived from the WS or laer ecotypes and therefore may contain polymorphisms when compared to sequences from Col-0. Genet carried out the library production and sequencing of the full-length clones. Ceres, Inc. carried out the clustering of the 5' sequences, selection of clones, and sequence assembly. | | |
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| | /organism="Arabidopsis thaliana" | | |
| | /db_xref="taxon:3702" | | |
| | /clone="17909" | | |
| BASE COUNT | 583 a 566 c 483 g 692 t | | |
| ORIGIN | | | |
| Query Match: | 69.0% | Score 1341.2; | DB 8; Length 2324; |
| Best Local Similarity | 82.8% | Pred. No. 8.3e-260; | |


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QY 910 CAGTTGAAAGTTGGAGTGGTTCAGGAGAGAGGGAGTTTCAGGACAGAGTGTGAGATCATC 969
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RESULT 11
AB020746
LOCUS

AB020746 79706 bp DNA linear PIN 27-DEC-2000

DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE

Arabidopsis thaliana genomic DNA, chromosome 3, p1 clone: MOB24.
AB020746 BAB00014
Version AB020746.1 GI:3985949

ORGANISM

Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsids.

REFERENCE
AUTHORS
TITLE

1 (sites)
Kaneko, T., Katoh, T., Sato, S., Nakamura, A., Asamizu, E. and Tabata, S.
Structural analysis of Arabidopsis thaliana chromosome 3. II.
Sequence features of the 4,251,895 bp regions covered by 90 p1, TAC
and BAC clones
DNA Res. 7 (3), 217-221 (2000)

JOURNAL
MEDLINE
REFERENCE

2 (bases 1 to 79706)
Kaneko, T., Katoh, T., Sato, S., Nakamura, Y., Asamizu, E. and Tabata, S.
Direct Submission
Submitted (03-DEC-1998) Yasukazu Nakamura, Kazusa DNA Research
Institute, Department of Plant Gene Research; 1532-3, Yana,
Kisarazu, Chiba 292-0812, Japan (E-mail: ynakam@kazusa.or.jp,
Tel: 81-438-52-3935, Fax: 81-438-52-3934)

AUTHORS

Address for correspondence: kaos@kazusa.or.jp
For the latest information on annotation of this clone, please see
http://www.kazusa.or.jp/kaos/cgi-bin/sgd-graph.cgi?c=MOB24

COMMENT

Genes with similarity to proteins in the databases are described in
'product' or 'note' qualifiers. Genes that have no significant
protein similarity are described as 'unknown protein'.
The software programs used to predict genes include: Grail
(Informatics Group, Oak Ridge National Laboratory,
http://compbio.ornl.gov/Grail-1.3//),
GENSCAN (Chris Burge, MIT, http://CCR-081.mit.edu/GENSCAN.html),
NetGene2 (S.M. Hebsgaard, et al., CBS, Technical University of
Denmark, http://www.cbs.dtu.dk/services/NetGene2/) and
SplicePredictor (Volkert Brendel, Stanford University,
http://greenlab.zool.iastate.edu/cgi-bin/sp.cgi).
Genes encoding tRNAs are predicted by tRNAscan-SE
(Sean Eddy, Washington University School of Medicine, St. Louis,
http://genome.wustl.edu/eddy/tRNAscan-SE/).
This sequence may not be the entire insert of this clone. It may be
shorter because we remove overlaps between neighboring submissions.
The 5' clone is MXP5 and the 3' clone is MSD24.

FEATURES
Source

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CDS

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Db 1989 GAATAGAGGCTCAATGA 2006

RESULT 13
AX088884
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
AX088884
Sequence 9 from Patent WO0114563.
AX088884
AX088884.1 GI:3397647
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Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 2104)
Goring, D. and Silva, N.
Proline-rich extensin-like receptor kinases
Patent: WO 0114563-A 9 01-MAR-2001;
Goring, Daphne (CA); Silva, Nancy (CA)
Location/Qualifiers
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ORIGIN
Query Match 22.0%; Score 427.2; DB 6; Length 2104;
Best Local Similarity 61.8%; Pred. No. 9.1e-76;
Matches 790; Conservative 0; Mismatches 413; Indels 75; Gaps 4;
QY 681 TCACACACCCCTTTCATGAGCAGCAGCGCGGCTCGGACTACTCGGACCGTCCAGTCT 740
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ACCESSION AX088887
VERSION AX088887.1 GI:13397650
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE 1 (bases 1 to 2261)
Goring, D. and Silva, N.
Proline-rich extensin-like receptor kinases
TITLE Patent: WO 0114563-A 12 01-MAR-2001;
JOURNAL Goring, Daphne (CA); Silva, Nancy (CA)
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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ALIGNMENTS

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ID AAAT7094 standard; DNA; 1944 BP.

XX AAAT7094;

XX AAAT7094;

DT 17-MAR-2001 (first entry)

DE Brassica napus PERK1 DNA.

XX Proline-rich extensin-like receptor kinase; PERK; resistance; plant; ds.

XX Brassica napus.

XX WO200114563-Al.

XX 01-MAR-2001.

XX 18-AUG-2000; 2000WO-CA00966.

XX 19-AUG-1999; 99US-0149466.

XX 13-OCT-1999; 99US-0159122.

XX (GORI/) GORING D.

XX (SILV/) SILVA N.

XX Goring D, Silva N;

XX WPI; 2001-244305/25.

XX New proline-rich, extensin-like receptor kinase nucleic acids and

PT polypeptides useful for increasing plant wounding or pathogen
 PT resistance, or for producing transgenic plants with increased wounding
 PT or pathogen resistance -

XX Claim 6; Fig 1; 91pp; English.

XX The present invention relates to proline-rich extensin-like
 CC receptor kinase (PERK). The PERK nucleic acids and polypeptides
 CC are useful for increasing the resistance of plants to wounding
 CC and pathogens. These are also useful for producing transgenic
 CC plants with increased wounding and pathogen resistance compared
 CC with a wild type plant, as well as in assays for identifying
 CC and developing compounds to inhibit and/or enhance polypeptide
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Query Match 100.0%; Score 1944; DB 22; Length 1944;
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KW      protein identification; signal transduction pathway;
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| DB | 389 | TTTCTAGTAGAAGTTCTCATGCTCAGCTTACTACATCATCAAACTGTTATTTGTT | 448 | 389 | TTTCTAGTAGAAGTTCTCATGCTCAGCTTACTACATCATCAAACTGTTATTTGTT |
| QY | 1006 | GGTTATTCATGCGCGGTGCCAAAGATTCGTGTCTATGAGTTTGTCTTCAACAAAT | 1065 | 1006 | GGTTATTCATGCGCGGTGCCAAAGATTCGTGTCTATGAGTTTGTCTTCAACAAAT |
| DB | 449 | GGTTATTCGTGTGAGAGCAGAGCTTCTGTTTATGATATATGATATGCTTCTGATCA | 508 | 449 | GGTTATTCGTGTGAGAGCAGAGCTTCTGTTTATGATATATGATATGCTTCTGATCA |
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| DB | 569 | ATGAAGATTCAGCAGGTGCTGCCAAGAGCTGGAGTACCTTCATGACAAAGCTATCA | 528 | 569 | ATGAAGATTCAGCAGGTGCTGCCAAGAGCTGGAGTACCTTCATGACAAAGCTATCA |
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| QY 859 | GGTATGCTGCACAAAGGTGTGTCGTCAGTGGGAAAGAGTTCTCTGTGAAGAGAGTGA | 918 | | |
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| QY 919 | GTGGGAGTGGCTCAGGAGGAGGAGGAGTTCAGGCGAGAGGTTGAGATCATCAGCAGATT | 978 | | |
| Db 574 | AAACAAGGGGTCACTGAAAGAGGAGTTTAGAGTGAAGTGAAGCTATCGGGCGGTGA | 633 | | |
| QY 979 | CACCACAGGCATCTGCTGTCCTGTTGTTTATGATCGCCCTGTCACAAAGATTGCTT | 1038 | | |
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| QY 1039 | GTCATAGTGTGCTCTACACACATCTCGAGCTTCACTCCATGCGAGGAGCGGCT | 1098 | | |
| Db 694 | GTGATGACTGCTGATATGCGAACTTGGAGCAATGGATTCATGGGATGTTGGTGT | 753 | | |
| QY 1099 | ACAA-----TSGAATGGAGCACCAGATGAAGATTGCTCTTGGATCTGCTAAGGACTT | 1152 | | |
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979 GCTAAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1038
QY 1321 TACTTGGCTCGGTAATGCTGCAAGCGGAAAGCTCAGGAGAGTCTGACGTTTCTCA 1380
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RESULT 8
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AC AAC45313;
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DT 18-OCT-2000 (first entry)
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DE Arabidopsis thaliana
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XX Hybridisation assay; genetic mapping; gene expression control;
XX protein identification; signal transduction pathway;
XX metabolic pathway; promoter; termination sequence; ss.
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XX Arabidopsis thaliana.
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XX EF1033405-A2.
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Query Match 10.1%; Score 197.2; DB 21; Length 1751;
Best Local Similarity 57.7%; Pred. No. 4.4e-37;
Matches 374; Conservative 0; Mismatches 268; Indels 6; Gaps 1;

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QY 847 CAAAGCGGGTTCGGTTACGCTCACAAAGGTGTGTGCTAGTGGCTAGTAAAGAGATGTTGCTGTG 906
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QY 907 AACCAAGTGAAGTTGGAGTGTGTCAGGGAGAGAGGAGTTTCAGGCAGAGGTTGATC 966
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DB ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
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RESULT 9
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DT 17-OCT-2000 (first entry)
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DE
XX
KW Hybridisation assay; genetic mapping; gene expression control;
XX protein identification; signal transduction pathway;
XX metabolic pathway; promoter; termination sequence; ss.
OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
XX
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PR 09-MAR-1999; 99US-0123548.
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QY 907 AACGAGTTGAAAGTTGGAGTGGTTCAGGAGAGAGGGAGTTTCAGGCGAGAGTTGAGATC 966
Db 640 AAGAATCTCTTACCAACAAGGTCAGCGGAGAGGAGTTCAAAAGTTGAAGTAGAAGCA 699
QY 967 ATCAGAGAGTTCACACAGCATCTGGTGTCTCTTGTGTGTTATTCATCGCCGGTGC- 1025
Db 700 ATGGGAAGTGAACATAGAAAGTGTGGTGTCTGATGGGATATTTGCTGACAGTGTCT 759
QY 1026 -----CAAAAGATTCGTTGTCTATGAGTTTGTCTTAACAACAATCTCGAGCTTCACCTC 1080
Db 760 CAAGTCAAGGATGCTTGTCTATGATATATTAATGATGAACTGGAGCACTGGTTA 819
QY 1081 CATGGCGAGGAGCGGCC-----TACAAATGGAATGGAGCACAGATTAAGATTGCTCTT 1134
Db 820 CACGGTCACTAGTCCGGTGAGTCTCTTACGFGGAGATACCGCATGAAGATAGCCATT 879
QY 1135 GGATCTCTTAAGAGACTTCTTATCTCAAGAGATTCGAATCTCAATCAATCAATCACCGT 1194
Db 880 GGAACAGCAAGAGATTAGCTATTTTACAGAGGGCTTGAACCTTAAGGTTGTCAACCGT 939
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PR 21-OCT-1999; 99US-0160768.
PR 21-OCT-1999; 99US-0160770.
PR 21-OCT-1999; 99US-0160814.
PR 21-OCT-1999; 99US-0160815.
PR 22-OCT-1999; 99US-0160980.
PR 22-OCT-1999; 99US-0160981.
PR 22-OCT-1999; 99US-0160989.
PR 25-OCT-1999; 99US-0161404.
PR 25-OCT-1999; 99US-0161405.
PR 25-OCT-1999; 99US-0161406.
PR 26-OCT-1999; 99US-0161359.
PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161992.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

Query Match 10.0%; Score 194.6; DB 21; Length 1674;
Best Local Similarity 55.9%; Pred. No. 1.8e-36;
Matches 415; Conservative 0; Mismatches 319; Indels 9; Gaps 2;

QY 782 GCACCTTCACATACGAGGAGTAGCTAGAGCCACCAATGTTTCGCCAGGCGACITGT 841
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 553 GGAGCTTCACGTTCAAGGAGTTAGCTGCAGCTACAAGAACTCCGGGAAGTTAATTGC 612
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 842 TAGCACAAAGCGGGTTCGGTTACGTCACAAAGGTGTTCCCTAGTAGGGGAAGATTG 901
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 613 TCGGAGAAGGAGGAGTTTGGCAGAGTTTATAGAGGACGTTTAGATTACAGCAAGTAGTG 672
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 902 CTGTGGAAGCAGTTGAAAGTTGGGAGTGTGTCAGGAGAGAGGAGTTTCAGGCAGAGGTTG 961
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 673 CTATTAGCAATTGAATCCAGATGGGCTTCAAGGGAACCGAGAGTTTATAGTAGAGTTC 732
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 962 AGATCATCAGCAGAGTTCCACACAGGAGCATGTTGTTCTCTGTTGGTATTGATGCGCG 1021
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 733 TTATGCTTAGCTTATTGCAATCATCCCAATCTCGTTACATTGATCGGTACTGTACTCTG 792
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1022 GTGCCAAAGATTCCTTGTCATAGAGTTTGTTCCTACACAAATCTCGAGCTTCACTT 1079
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 793 GTGATCAAGAGACTTCTTGCTATGAATACATGCAATGGGAAGCTTAGAAGATCACCTTT 852
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1080 ---CCATGGGAGGAGCGGCTACAATGGAATGGACACCAAGATTGAAGATTGCTCTTG 1135
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RESULT 13
AAAF77097
ID AAF77097 standard; DNA; 2820 BP.
XX
XX
AC AAF77097;
XX
XX 17-MAY-2001 (first entry)
XX
XX Arabidopsis gene #3.
XX
XX Proline-rich extensin-like receptor kinase; PERK; resistance;
XX plant; ds.
XX
XX Arabidopsis thaliana.
XX
XX WO200114563-A1.
XX
XX 01-MAR-2001.
XX
XX 18-AUG-2000; 2000WO-CA00966.
XX
XX 19-AUG-1999; 99US-0149466.
XX
XX 13-OCT-1999; 99US-0159122.
XX
XX (GORI/) GORING D.
XX (SILV/) SILVA N.
XX
XX Goring D, Silva N;
XX
XX WPI; 2001-244305/25.
XX
XX New proline-rich, extensin-like receptor kinase nucleic acids and
XX polypeptides useful for increasing plant wounding or pathogen
XX resistance, or for producing transgenic plants with increased wounding
XX or pathogen resistance -
XX
XX Examples; Fig 13; 9lpp; English.
XX
XX The present invention relates to proline-rich extensin-like
XX receptor kinase (PERK). The PERK nucleic acids and polypeptides
XX are useful for increasing the resistance of plants to wounding
XX and pathogens. These are also useful for producing transgenic
XX plants with increased wounding and pathogen resistance compared
XX with a wild type plant, as well as in assays for identifying
XX and developing compounds to inhibit and/or enhance polypeptide
XX function directly.
XX
XX Sequence 2820 BP; 819 A; 629 C; 577 G; 795 T; 0 other;

Query Match 9.9%; Score 192.2; DB 22; Length 2820;
Best Local Similarity 67.2%; Pred. No. 8.2e-36;
Matches 272; Conservative 0; Mismatches 133; Indels 0; Gaps 0;

QY 681 TCACACACCGCTTTCATGAGCAGCAGCGCGCTCCGACTACTCGACCGTCCAGTTCT 740
DQ ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 977 TCACAGACACCGCTGTCGTGGTCTCAGAGTGAIGTTCACACTTAACCGGTGCACTGC 1036
QY 741 TCTTCCACCGCTCCACGGGCTTGTTAGGCTTCTCCAAAGCACTTTCACATCAGGGA 800
DQ ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1037 TATACCGTCACTCAAGTGCACACTCTTGTCACACACCAAGCACTTTCATACATGATGA 1096
QY 831 GCTAGTAGAGCCACCAATGGTTTCGAGGCGGACTGTGTTAGGCAAGCGGGTTCGG 860
DQ ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1097 ACTGTCATGCAACAGAGGTTTCGCTCAGTCAAAATTTGCTAGGACAAAGGATTTGG 1156
QY 861 TTACGTGCAAAAGGTGTGCTAGTGGGAAGGTTGCTGTCAGCAGTTGAAGT 920
DQ ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1157 STATGTTCAATAGAGGAGTTTCGCTAGTGGCAAGGATTTGAGTGAAGAGTCTTAAC 1216
QY 921 TGGAGTGTGTCAGGAGGAGGAGTTTCAGGACAGAGTTGATCATCAGCAGAGTTCA 980
DQ ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1217 TGGAGTGCACAGGAGGAGGAGTTTCAGCAGAGGTTGATCATCAGGAGTTCA 1276
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QY 981 CCACAGGATCGTGTCTCTCTGTTGGTTATTGTCATCGCCGTCACCAAGATTTGCTT 1040
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1277 TCATCGTCATCGTGTGTTCTCTGTTGGATGATTTGTCATCTGTCGAAGACTTTTGT 1336
QY 1041 CTATGAGTTTTCCTAACCAAACTCTGAGCTTCACCTCCCATGG 1085
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1337 TTATGAGTTTATACCTAACACACTCTTGAATTCATCTCATGG 1381

RESULT 14
AAAF77096
ID AAF77096 standard; DNA; 2520 BP.
XX
XX AC AAF77096;
XX
XX 17-MAY-2001 (first entry)
XX
XX Arabidopsis gene #2.
XX
XX Proline-rich extensin-like receptor kinase; PERK; resistance;
XX plant; ds.
XX
XX Arabidopsis thaliana.
XX
XX WO200114563-A1.
XX
XX 01-MAR-2001.
XX
XX 13-AUG-2000; 2000WO-CA00966.
XX
XX 19-AUG-1999; 99US-0149466.
XX
XX 13-OCT-1999; 99US-0159122.
XX
XX (GORI/) GORING D.
XX (SILV/) SILVA N.
XX
XX Goring D, Silva N;
XX
XX WPI; 2001-244305/25.
XX
XX New proline-rich, extensin-like receptor kinase nucleic acids and
XX polypeptides useful for increasing plant wounding or pathogen
XX resistance, or for producing transgenic plants with increased wounding
XX or pathogen resistance -
XX
XX Examples; Fig 12; 9lpp; English.
XX
XX The present invention relates to proline-rich extensin-like
XX receptor kinase (PERK). The PERK nucleic acids and polypeptides
XX are useful for increasing the resistance of plants to wounding
XX and pathogens. These are also useful for producing transgenic
XX plants with increased wounding and pathogen resistance compared
XX with a wild type plant, as well as in assays for identifying
XX and developing compounds to inhibit and/or enhance polypeptide
XX function directly.
XX
XX Sequence 2520 BP; 717 A; 553 C; 537 G; 713 T; 0 other;

Query Match 9.9%; Score 192; DB 22; Length 2520;
Best Local Similarity 70.8%; Pred. No. 8.8e-36;
Matches 255; Conservative 0; Mismatches 105; Indels 0; Gaps 0;

QY 730 CGTCCAGTTCTCTCCACCGTCTCCAGGCTTGTTAGGCTTCTCCAAAGCACTTTC 789
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 841 CGCCAGTTTACTCTCTCTCCCTGCTCTAGCCCTCGATTCACACAGACACTTTT 900
QY 790 ACATACAGGAGCTAGTAGACCCCAATGGTTTCTCCGAGGCGAATTTGTTAGGACAA 849
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 901 ACTTACCAAGAGCTTGGGCTGCAACAGGAGGTTTACGGATGCTAACCTTTTGGACAG 960
QY 850 GCGGGGTTGCTTACGTGCAACAGGAGTTCCTGCTAGTGGGAAGGTTGCTGCTGAG 909
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
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Db 961 GGAGGATTTGGGTATGTCCATAAAGGAGTCTTCCTAGCGGGAAGAGTAGCAGTTAAG 1020
QY 910 CAGTTGAAAGTTGGGAGTGGTCCAGGAGAGAGAGGAGTTTCAGGCAGAGTTTGAGATCATC 969
Db 1021 AGTTTAAAGCGGTAGCGGACAGAGAGAGAGGAGGAGTTTCAGCTGAGGTCGATATCATT 1080
QY 970 ACAGAGTTTCACACAGGAGCATCTGGTGTCTCTTGTGTTATGTCATCCGCGTGCCAAA 1029
Db 1081 ACCCTGTGCATCATCGGTATCTTGTCTTGGTTGGATATGTCATAGTGATGGACAG 1140
QY 1030 AGATTGCTGTCTATGAGTTTCTCTTACACAAATCICGAGCTTCACTCCATGGCGAG 1089
Db 1141 AGAGTTGGTTATGAGTTTCTCTTACAAACATTTGGAATATCATCTTCATGTTAG 1200

RESULT 15
AAC50527
ID AAC50527 standard; DNA; 1848 BP.
XX AAC50527;
AC AAC50527;
XX
DF 18-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 65175.
XX
KW Hybridisation assay; genetic mapping; gene expression control;
KW protein identification; signal transduction pathway;
KW metabolic pathway; promoter; terminator; termination sequence; ss.
XX
OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-0301439.
XX
PR 25-FEB-1999; 99US-0121825.
PR 05-MAR-1999; 99US-012180.
PR 09-MAR-1999; 99US-0123548.
PR 23-MAR-1999; 99US-0125788.
PR 25-MAR-1999; 99US-0126264.
PR 29-MAR-1999; 99US-0126785.
PR 01-APR-1999; 99US-0127462.
PR 06-APR-1999; 99US-0128234.
PR 08-APR-1999; 99US-0128714.
PR 15-APR-1999; 99US-0129845.
PR 19-APR-1999; 99US-0130077.
PR 21-APR-1999; 99US-0130449.
PR 23-APR-1999; 99US-0130510.
PR 28-APR-1999; 99US-0130891.
PR 28-APR-1999; 99US-0131449.
PR 30-APR-1999; 99US-0132048.
PR 30-APR-1999; 99US-0132407.
PR 04-MAY-1999; 99US-0132484.
PR 05-MAY-1999; 99US-0132485.
PR 06-MAY-1999; 99US-0132486.
PR 07-MAY-1999; 99US-0132487.
PR 07-MAY-1999; 99US-0132863.
PR 11-MAY-1999; 99US-0134256.
PR 14-MAY-1999; 99US-0134218.
PR 14-MAY-1999; 99US-0134219.
PR 14-MAY-1999; 99US-0134221.
PR 14-MAY-1999; 99US-0134370.
PR 18-MAY-1999; 99US-0134768.
PR 19-MAY-1999; 99US-0134941.
PR 20-MAY-1999; 99US-0135124.
PR 21-MAY-1999; 99US-0135353.
PR 24-MAY-1999; 99US-0135629.
PR 25-MAY-1999; 99US-0136021.
PR 27-MAY-1999; 99US-0136392.
PR 28-MAY-1999; 99US-0136782.
PR 01-JUN-1999; 99US-0137222.
PR 03-JUN-1999; 99US-0137528.
PR 04-JUN-1999; 99US-0137502.
PR 07-JUN-1999; 99US-0137724.
PR 08-JUN-1999; 99US-0138094.
PR 10-JUN-1999; 99US-0138540.
PR 10-JUN-1999; 99US-0138847.
PR 14-JUN-1999; 99US-0139119.
PR 16-JUN-1999; 99US-0139452.
PR 16-JUN-1999; 99US-0139453.
PR 17-JUN-1999; 99US-0139492.
PR 18-JUN-1999; 99US-0139454.
PR 18-JUN-1999; 99US-0139455.
PR 18-JUN-1999; 99US-0139456.
PR 18-JUN-1999; 99US-0139457.
PR 18-JUN-1999; 99US-0139458.
PR 18-JUN-1999; 99US-0139459.
PR 18-JUN-1999; 99US-0139460.
PR 18-JUN-1999; 99US-0139461.
PR 18-JUN-1999; 99US-0139462.
PR 18-JUN-1999; 99US-0139463.
PR 18-JUN-1999; 99US-0139750.
PR 18-JUN-1999; 99US-0139763.
PR 21-JUN-1999; 99US-0139817.
PR 22-JUN-1999; 99US-0139899.
PR 23-JUN-1999; 99US-0140353.
PR 23-JUN-1999; 99US-0140354.
PR 24-JUN-1999; 99US-0140695.
PR 28-JUN-1999; 99US-0140823.
PR 29-JUN-1999; 99US-0140991.
PR 30-JUN-1999; 99US-0141287.
PR 01-JUL-1999; 99US-0141842.
PR 02-JUL-1999; 99US-0142154.
PR 06-JUL-1999; 99US-0142390.
PR 08-JUL-1999; 99US-0142803.
PR 09-JUL-1999; 99US-0142920.
PR 12-JUL-1999; 99US-0142977.
PR 13-JUL-1999; 99US-0143542.
PR 14-JUL-1999; 99US-0143624.
PR 15-JUL-1999; 99US-0144005.
PR 16-JUL-1999; 99US-0144085.
PR 16-JUL-1999; 99US-0144086.
PR 19-JUL-1999; 99US-0144325.
PR 19-JUL-1999; 99US-0144331.
PR 19-JUL-1999; 99US-0144332.
PR 19-JUL-1999; 99US-0144333.
PR 19-JUL-1999; 99US-0144334.
PR 19-JUL-1999; 99US-0144335.
PR 20-JUL-1999; 99US-0144352.
PR 20-JUL-1999; 99US-0144632.
PR 20-JUL-1999; 99US-0144884.
PR 21-JUL-1999; 99US-0144814.
PR 21-JUL-1999; 99US-0145086.
PR 21-JUL-1999; 99US-0145088.
PR 22-JUL-1999; 99US-0145085.
PR 22-JUL-1999; 99US-0145087.
PR 22-JUL-1999; 99US-0145089.
PR 22-JUL-1999; 99US-0145192.
PR 23-JUL-1999; 99US-0145145.
PR 23-JUL-1999; 99US-0145218.
PR 23-JUL-1999; 99US-0145224.
PR 26-JUL-1999; 99US-0145276.
PR 27-JUL-1999; 99US-0145913.
PR 27-JUL-1999; 99US-0145918.
PR 27-JUL-1999; 99US-0145919.
PR 28-JUL-1999; 99US-0145951.
PR 02-AUG-1999; 99US-0146386.
PR 02-AUG-1999; 99US-0146388.
PR 02-AUG-1999; 99US-0146389.
PR 03-AUG-1999; 99US-0147038.
PR 04-AUG-1999; 99US-0147204.
PR 04-AUG-1999; 99US-0147302.
PR 05-AUG-1999; 99US-0147192.
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TYPE: DNA
ORGANISM: Brassica napus
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(2189)
OTHER INFORMATION:
US-10-086-464-3

Query Match 100.0%; Score 1944; DB 9; Length 2189;

Best Local Similarity 100.0%; Pred. No. 0;
Matches 1944; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGTCCTCGGCGCGCTCCCGGAGCTGTTCCGCTCCATCTCCACCACTCAACTCCACA 60
DB 97 ATGTCCTCGGCGCGCTCCCGGAGCTGTTCCGCTCCATCTCCACCACTCAACTCCACA 156
QY 51 ACCACCACTCTCTCCAGCTTCGCTCTCTCTCCACCACTCTCTCTCTCTCTCTCTCT 120
DB 157 ACCACCACTCTCTCCAGCTTCGCTCTCTCTCTCCACCACTCTCTCTCTCTCTCTCT 216
QY 121 CCATCCACTATTCGACATCT 180
DB 157 CCATCCACTATTCGACATCT 276
QY 181 CCATCTCCACCACT 240
DB 277 CCATCTCCACCACT 336
QY 241 CCCTCTCACTAGCGCGGATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 300
DB 337 CCCTCTCACTAGCGCGGATCT 396
QY 301 CCACCTTCAGTCCGAGGACCACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 360
DB 397 CCACCTTCAGTCCGAGGACCACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 456
QY 361 CCATCT 420
DB 457 CCATCT 516
QY 421 GGAATCGCACTCGAGAGTCT 480
DB 517 GGAATCGCACTCGAGAGTCT 576
QY 481 AAGAAGAAACGACGAGAGCAAGAGATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 540
DB 577 AAGAAGAAACGACGAGAGCAAGAGATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 636
QY 541 GTTCCCAAGCGGAGGACCTTACGCTGGAGACGACCAACAAATGGCGSCAACAAGCA 600
DB 637 GTTCCCAAGCGGAGGACCTTACGCTGGAGACGACCAACAAATGGCGSCAACAAGCA 696
QY 601 ACACCACTGATATGCTGACCT 660
DB 597 ACACCACTGATATGCTGACCT 756
QY 661 CCACGGCAACTCTCTCACTCTCACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 720
DB 757 CCACGGCAACTCTCTCACTCTCACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 816
QY 721 TACTCGGACCTGATCT 780
DB 817 TACTCGGACCTGATCT 876
QY 781 AGCACTTTCATACAGGAGTCTAGAGTCTAGAGTCTAGAGTCTAGAGTCTAGAGTCTAG 840
DB 877 AGCACTTTCATACAGGAGTCTAGAGTCTAGAGTCTAGAGTCTAGAGTCTAGAGTCTAG 936
QY 841 TTAGACAAGCGGCTTCT 900
DB 937 TTAGACAAGCGGCTTCT 996
QY 901 GCTGTGAAGCAGTTGAAAGTTGGAGTGGTTCAGGAGAGAGGAGTTTTCAGGAGAGGTT 960

RESULT 3

Db 1791 ACAGCACTAGAGGAGATATGTCAATGATGATCTAAGTCAGGGAACAGACAGGACA 1850
 QY 1695 AAGCAATGTATACAGCTCATACGAGGAAGCAGCAGATATGACTCGAGCCAGTACATGA 1754
 Db 1851 AAGCACAGTACTGAGCCCGGAGCGGTGAGCTCAGAGTATGACCAAGCTCGTACACGGC 1910
 QY 1755 AGACATGAAGAAGTTTAGGAAATGGCACTTGGAACTCAAGAGTACACGCGCAGGSGGA 1814
 Db 1911 AGACATGAAGAAGTTTCAAGAACTGGGCTTAGAGAAATCAAGCACTG----- 1966
 QY 1815 GTACAGTAATCCGACCACTGACTATGAGCTGTACCCGTCTGGTTTCAAGCAGCGAGGSCCA 1874
 Db 1967 --AATGTTGGGAACAAGTGAATGATGCTTAAACCCCTTCTGCTTCAAGTAGTGAAGAAAT 2024
 QY 1875 AACCAACAGCGCAATGGA 1892
 Db 2025 GAATAGAGGCTCAATGAA 2042

RESULT 7

US-10-086-464-16
 ; Sequence 16, Application US/10086464
 ; Publication No. US20020199218A1
 ; GENERAL INFORMATION:
 ; APPLICANT: GORING, Daphne R. et al.
 ; TITLE OF INVENTION: PROLINE-RICH EXTENSIN-LIKE RECEPTOR KINASES
 ; FILE REFERENCE: P 25,762-A USA
 ; CURRENT APPLICATION NUMBER: US/10/086,464
 ; CURRENT FILING DATE: 2002-02-28
 ; PRIOR APPLICATION NUMBER: US 10/069,304
 ; PRIOR FILING DATE: 2002-02-19
 ; PRIOR APPLICATION NUMBER: PCT/CA00/00966
 ; PRIOR FILING DATE: 2000-08-18
 ; PRIOR APPLICATION NUMBER: US 60/149,466
 ; PRIOR FILING DATE: 1999-08-19
 ; PRIOR APPLICATION NUMBER: US 60/159,122
 ; PRIOR FILING DATE: 1999-10-13
 ; NUMBER OF SEQ ID NOS: 27
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 16
 ; LENGTH: 2196
 ; TYPE: DNA
 ; ORGANISM: Arabidopsis thaliana
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (1)..(2196)
 ; US-10-086-464-16

Query Match 21.3%; Score 413.6; DB 9; Length 2196;
 Best Local Similarity 67.0%; Pred. No. 1.2e-109;
 Matches 606; Conservative 0; Mismatches 289; Indels 9; Gaps 1;
 QY 782 GCACCTTTCATACAGGAGCTAGCTAGAGCCACCAATGGTTCTCGAGCGCACTGT 841
 Db 1124 GAATGTCTCTACGAAGAACTTCAAAAGCACTGGTGGATTTTCAGAGGAGAACCTTT 1183
 QY 842 TAGCAGACGGGTTCCGTTACCTGCACAAAGTGTGTTCCCTAGTGGGAAAGACTTG 901
 Db 1184 TGGGAAGAGCGGTTCCGATATTTTCAAAAGGAGTGTTCAAAACGGGACAGAACTTG 1243
 QY 902 CTGTGAAGCAGTTGAAGTTGGGAGTGGTCAGGAGAGAGGAGCTTTCAGGACAGGTTG 961
 Db 1244 CGGTGAGCAGCTGAAGATTGGGAGCTATCAAGGGAAGAGAAATTCAGCTAGGTTG 1303
 QY 962 AGATCATCAGCAGAGTTACACACAGGCACTGGTCTCTCTTTGTTGGTTATTCATCGCCG 1021
 Db 1304 ACACAAICAGTAGGGTTTCATCAATGAAGCACCTCGTTCATTGTTGGTTATTGCGTTAATG 1363
 QY 1022 GTGCCAAAAGATTGCTGTCTATGAGTTTGTTCGCAACAACTCTCGAGCTTCACTCC 1081
 Db 1364 GAGATTAAGAGACTCTTGGTTTACAGTTTGTTCCTAAAGATACCTTGGAGTTCACCTGC 1423
 QY 1082 ATGGCGAGGGAGCGGCTTCAATGAATGGAATGGAGCACCAAGATTGAAGATTGCTCTTGATCTG 1441

Db 1424 ATGACAACAGAGAGAGCGTGTGGATGGGAATGAGGCTCAGGATTCGTAGGAGCAG 1483
 QY 1142 CTAAGAGACTTCTCTATCTTCATGAAGATTGCAATCTCTAAATCAATCACTACCTGATATCA 1201
 Db 1484 CAAAAGGATTAGCTTATCTTCACTGAGGATTGCGAGTCCAACTATAATTCACCTGATATCA 1543
 QY 1202 AGGCTTCAACATATTGATAGATTTCAGTTTTCAGCTAAGCTTCTGATTTTGGTCTTG 1261
 Db 1544 AAGCAGCTAATATCCTTCTAGATTCCAAATTTGAGGCAAGGCTCTCTGACTTTGGACTAG 1603
 QY 1262 CTAAGATTGCTTCTCATACAAA-----CAGCATCTATCAACACCTGTGATGGGAA 1312
 Db 1604 CCAAGTTTCTCAGACACCAATTCATTCATCTACTCTACTCGAGTGGTAGGAA 1663
 QY 1313 CTTTGGGTACTTGGCTCCGGAATACGCTGCAAGCGGAAAGCTCAGGAGAAAGTCTGACG 1372
 Db 1664 CTTTCGGATACATGGCTCCAGAAATACGGCTCCAGTGGTAAAGTAACTGATAAATCAGATG 1723
 QY 1373 TTTTCTCATTTGGCGTTGTGCTTTTGGAGCTCAATTACTGGAGTCCGCCCTTGATGCCA 1432
 Db 1724 TATATTCCTTTGGGTCGTGCTTCTAGAACTCATCACTGGAGCTCCATCAATTTTGGCCA 1783
 QY 1433 ACAATGCTATGTAGATGACAGCTTAGTTGACTGGGACAGCAGCATTCGTTAAACCGAGCAT 1492
 Db 1784 AAGATCTCTCCACAACACAGAGTTTAGTAGACTGGCGAGGCCATTCCTTACGAAGCAA 1843
 QY 1493 CTGACAAAGGAGACTTTTGGGTTTGGCTGTAGCTGATGCAAGAAGTAAATAGTGGTATGACAGAG 1552
 Db 1844 TCCTCGGAGAAAGTTTGTGACTTCTTGTAGACTCAAGGTTGGAGAAGAATTACGATACAA 1903
 QY 1553 AGGAGATGGCTCGCATGGTTGCTTGTGCTGGCGCTTGTGTCGCCATTCAGCTCCGCCA 1612
 Db 1904 CTCAGATGGCAAAACATGGCTGCTGTGCTGCTTGTGATGATGCAATCAGCTTGGCTTC 1963
 QY 1613 GACCTCGCATGAGCCAGATTTGCTGCTGTGCTTGAAGAGAAATATATCACTGTCTGATCTTA 1672
 Db 1964 GGCCTAGAAATGAGCCAGTACTGATGCTCTCTTGAAGGCGAGGTGGCCCTGAGAAAGTGG 2023
 QY 1673 ACGA 1676
 Db 2024 AAGA 2027

RESULT 8

US-10-086-464-15
 ; Sequence 15, Application US/10086464
 ; Publication No. US20020199218A1
 ; GENERAL INFORMATION:
 ; APPLICANT: GORING, Daphne R. et al.
 ; TITLE OF INVENTION: PROLINE-RICH EXTENSIN-LIKE RECEPTOR KINASES
 ; FILE REFERENCE: P 25,762-A USA
 ; CURRENT APPLICATION NUMBER: US/10/086,464
 ; CURRENT FILING DATE: 2002-02-28
 ; PRIOR APPLICATION NUMBER: US 10/069,304
 ; PRIOR FILING DATE: 2002-02-19
 ; PRIOR APPLICATION NUMBER: PCT/CA00/00966
 ; PRIOR FILING DATE: 2000-08-18
 ; PRIOR APPLICATION NUMBER: US 60/149,466
 ; PRIOR FILING DATE: 1999-08-19
 ; PRIOR APPLICATION NUMBER: US 60/159,122
 ; PRIOR FILING DATE: 1999-10-13
 ; NUMBER OF SEQ ID NOS: 27
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 15
 ; LENGTH: 2261
 ; TYPE: DNA
 ; ORGANISM: Arabidopsis thaliana
 ; US-10-086-464-15

Query Match 21.3%; Score 413.6; DB 9; Length 2261;
 Best Local Similarity 67.0%; Pred. No. 1.3e-109;
 Matches 606; Conservative 0; Mismatches 289; Indels 9; Gaps 1;


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QY 782 GCACCTTTCACATGAGGAGCTAGAGCACCACCAATGTTCTCCAGGCGCACTTGT 841
Db 1151 GAATGTTCTCTACAGAACTTCAAAGCACTGGTGGATTTTCAGAGGAGCACTTT 1210
QY 842 TAGGACAAAGGGGTTGGTTACGTGCGCAAGAGTGTGCTCCAGTGGGAAAGATTG 901
Db 1211 TGGGAGAGGGGTTGGATATCTTCAAAAGGAGTGTGCAAAACGGGACAGAGTTG 1270
QY 902 CTGTGAACCACTTAAAGTTGGAGTGGTCAAGGAGAGAGGAGTTTCAGGACAGGTTG 961
Db 1271 CGGTCAAGCAGCTGAAGATTGGGAGCTATCAAGGAGAGAGAAATTCGAAGTGGTTG 1330
QY 962 AGATCATCAGCAGAGATTCAACACAGGATGCTCTCTGTTGGTTATTGCATCGCG 1021
Db 1331 ACACATCAGTAGGTTTCATCAAGCACCTGTTCTATGTTGGTTATTCGGTTAATG 1390
QY 1022 GTGCCAAAGATTGCTGTCTATGAGTTGTCTTAAACAATCTCGAGCTTCACCTCC 1081
Db 1391 GAGATAAAGACTCTTGTTTACGAGTTGTCTTAAAGATACCTTGGAGTTCCACTGC 1450
QY 1082 ATGCGGAGGAGCGCTACATGAGTGAAGTCAAGCAGGATTCAGATTCCTTGGATCG 1141
Db 1451 AIGAGACAGAGAGGAGGTTGGAATGGGAAAGAGGCTCAGGATTCCTAGGAGGAG 1510
QY 1142 CTAAAGGAGCTTCTTATCTTCATGAAGATTGCAATCCTTAAATCATTCACCGTGAATCA 1201
Db 1511 CAAAAGGATTAGCTTATCTTCATCAGGATTCAGTCCCACTATATTCACCGTGAATCA 1570
QY 1202 AGGCTTCAACATATGATGATTTCAAGTTTGAAGTTGAAGTTCGTGATTTGGTTG 1261
Db 1571 AAGCAGCTAATATCTCTAGATTCCAAATTTAGGCAAAAGGCTCTCTGACTTTGACTAG 1630
QY 1262 CTAAGATTGCTTCTGATACAAA-----CAGCATGTATCACAGCTGTATGGGAA 1312
Db 1631 CCAAGTTTCTCAGACACCACTTCACTATCTCATCTATCTCTACTCGAGTGGTAGGAA 1690
QY 1313 CTTTGGGACTTGGCTCCGGAATACGCTGGAAGGAAAGCTCACGGAGAGTCTGAGC 1372
Db 1691 CTTTGGGATACATGGCTCCAGATACGCTGCTCCAGTGGTAAAGTAACTATTAACAGATG 1750
QY 1373 TTTTCTCATTTGGGTTGTGCTTTTGGAGCTCATCTAGGAGCTGCGACCGCTTATGATGCA 1432
Db 1751 TATATCTTCTTGGGCTGCTGCTTCTAGAACTCATCTAGGAGCTCCATCAATTTTGGCCA 1810
QY 1433 ACATGCTATGTAGATGACAGCTTAGTGTAGCTGGCAGCAGCAATTCCTTAACCGAGCAT 1492
Db 1811 AAGATTCTCCACAAACAGAGTTAGTAGCTGGCAGGAGCCATTCCTTACGAAAGCAA 1870
QY 1493 CTGAGCAAGAGACTTTGAGGTTTAGCTGATGCAAGATGAATTAATGGGTATGACAGAG 1552
Db 1871 TCTCTGGAGAAAGTTTGGACTTCTTCTAGACTCAAGTTTGGAGAAAGATTAACGATACAA 1930
QY 1553 AGGAGATGCTCGCATGCTGCTGCTGGGTTGTTGTCGCGCATTCAGCTCGCGGCA 1612
Db 1931 CTCAGATGGCAAACTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1990
QY 1613 GACCTGCTGAGCAGGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1672
Db 1991 GGCCTAGAAAGCAGGATGAGTGGTCTTCTTGAAGCGGAGGTTGGCCCTGAGAAAGTTCG 2050
QY 1673 ACGA 1676
Db 2051 AAGA 2054
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RESULT 9

US-10-086-464-7

; Sequence 7, Application US/10086464

; Publication No. US20020199218A1

; GENERAL INFORMATION:

; APPLICANT: GORING, Daphne R. et al.

; TITLE OF INVENTION: PROLINE-RICH EXIENSIN-LIKE RECEPTOR KINASES

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; FILE REFERENCE: P 25,762-A USA
; CURRENT APPLICATION NUMBER: US/10/086,464
; CURRENT FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 10/069,304
; PRIOR FILING DATE: 2002-02-19
; PRIOR APPLICATION NUMBER: PCT/CA00/00966
; PRIOR FILING DATE: 2000-08-18
; PRIOR APPLICATION NUMBER: US 60/149,466
; PRIOR FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: US 60/159,122
; PRIOR FILING DATE: 1999-10-13
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 2196
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(2196)
; US-10-086-464-7
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Query Match 15.7%; Score 305.6; DB 9; Length 2196;
Best Local Similarity 59.1%; Pred. No. 3.6e-78;
Matches 644; Conservative 0; Mismatches 344; Indels 102; Gaps 3;

QY 786 TTTCATACAGGAGGAGCTAGTAGAGCCACCAATGTTCTCCAGGCGCACTTGTAGG 845
Db 1074 TTTCAGTTACGAGAGCTTGCTGAGATAACACAGGCTTGTCTCGCAAAACATCTTTGG 1133
QY 846 ACAAGCGGGTTCGCTTACGTCACAAAAGTGTGTGCCAGTGGGAAAGAGTTGCTGT 905
Db 1134 AGAAGCGGAGTTGGAATGTCTATTAAGTACATTCAGGATGTGAAGTTGTTCGGGT 1193
QY 906 GAAGCAGTTGAAGTTGGAGTGGTCAGGAGAGAGGAGTTTCAGGCGAGAGTTGAGAT 965
Db 1194 TAAGCAGCTTAAAGCTGGAAGTGGACAAAGTGACCGTGAATTCAAAGCAGAGTTGAGAT 1253
QY 966 CATCAGCAGAGTTCAACACAGGAGTGGTGTCTGTTGTTGTTGTTGTTGTTGTTGTTG 1025
Db 1254 CATCAGCGCGCTTCATCATCGCCATTTGCTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 1313
QY 1026 CAAAAGATTGCTTCTATGAGTTTCTTAAACAACATCTCGAGCTTCACCTCCATGG 1085
Db 1314 GCATAGATTTCTTATCTATGATAGTGTCTTAACTCAACCTTGGAGCAATTCGAT--- 1371
QY 1086 CGAGGAGCGGCTACAAATGGAATGGAGCACCAGATTGAAGATTGCTTGGATCTGCTAA 1145
Db 1372 -----GAGTGGTCTAAGAGAGTCCGGATCGCTATAGGATCAGCCAA 1412
QY 1146 AGGACTTCTTATCTTCATGAGATTGCAATCTCAATCTTAAATCTTCCCGTGATATCAAGGC 1205
Db 1413 AGGTTGGCATATCTTCAGAGAGCTGTCTCCGGAATTCATTCACAGAGATATAAAGTC 1472
QY 1206 TTCAACATATTTGATGAGATTCAAGTTTGAAGCTAAG----- 1242
Db 1473 AGCAATATTTCTTAGTAGATGATATGAAGCTCAGGCAATTAAGAAATCTCTCTTC 1532
QY 1243 -----GTTGCTGATTTTGGTCTTGTGCTTAAGATTGC 1271
Db 1533 GTTAAATCTATCTTATGACTGTAAAGTTTATGTTGCTGATTTTGGACTTGTAGACTCAA 1592
QY 1272 TTCTGATACAAACAGCATGTATCAACAGCTGTGATGGAGACCTTGGTGGTCTTGGCTCC 1331
Db 1593 TGATACAAACAAACTCATGTTTCAACTCGGGTTATGGGAACCTTCGGGTACCTAGCGCC 1652
QY 1332 GGAATAGCTGCAAGCGGAAAGCTCACGGAGAGTCTGACGCTTTTCTCATTTGGCGTTGT 1391
Db 1653 GGAATATGCTCAAGTGGAAATTCAGTATAGATCCGATGTATCTCATTCATTCGGGGTTGT 1712
QY 1392 GCTTTTGGAGCTCAATCTGACGCTGACCGGTTGATGCCAACAAATGTCTTAAGTAGATGA 1451
Db 1713 TCTCTTAGAGCTTGTAACTGACGGAACCAAGTTTGACGAGACTTCAGCCTCTAGGAGAAGA 1772
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RESULT 13
US-09-938-842A-1911
; Sequence 1911, Application US/09938842A
; Patent No. US20020160378A1
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeff
; APPLICANT: Kreps, Joel
; APPLICANT: Wang, Xun
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
; FILE REFERENCE: SAME, AND METHODS OF USE
; CURRENT APPLICATION NUMBER: US/09/938,842A
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/227,866
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/264,647
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/300,111
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO 1911
; LENGTH: 1353
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-938-842A-1911

Query Match 10.2%; Score 199; DB 9; Length 1353;
Best Local Similarity 56.9%; Pred. No. 3.1e-47;
Matches 406; Conservative 0; Mismatches 300; Indels 9; Gaps 2;

QY 799 GAGTACAGAGCCACCACATGTTCTCCGAGGCGACTTGTAGACAAAGCGGGTTC 858
DB 454 GAGCTTGAACACACTACTATGATGTTGTGAAGAGAAATGATCGGAGAGGAGGTAT 513
QY 859 GGTATCIGCACAAGAGTGTGCTAGTGGGAAGAAGTGTGTAAGACAGTGTGAAA 918
DB 514 GGGATGTTTATAGTGGGATTTAAGTATGAGTGGAACTAAGTGTGTCAGAAATCTGTT 573
QY 919 GTTGGAGTGGTCAGGAGAGAGGAGTTCAGSCAGAGTGTAGATCATCAGCAGAGTT 978
DB 574 AACACAGGGGTCAAGCTGAGAAGAGTGTAGAGTGAAGTGAAGTATCGGCGGTGA 633
QY 979 CACCAAGGATCTGGTCTCTCTGTGGTATGATGCTGATGCTGATGCTGATGCTG 1038
DB 634 AGGCATAAAGATCTGTTAGGCTATTAGGATATGCTGCTGAAGGAGCATACAGGATGCT 693
QY 1039 GTCTAGAGTGTCTTCTTACAAACAATCTCGAGCTTCACCTCCATGCGGAGGACGGCT 1098
DB 694 GGTATGACTACCTCGATATGTCACACTTGGAGCAATGATTCATGCGGATGTTGTGAT 753
QY 1099 ACAA-----TGGAAATGGAGCACAGATTTGAAGATGCTCTTGGATCTGTAAGGACTT 1152
DB 754 AAAAGTCCGTGACTTGGGATATTCGTATGAACATAATATCTTTCATGCGGAAAGATG 813
QY 1153 TCTTATCTCATAGATTCATCTCTTAAATCATTCACCGTGTATATCAGGCTTCAAC 1212
DB 814 GCCTATCTGATGGGCTCTTGACCCGAAAGTCTGTTCTGCGGACATAAATCTAGTAAT 873
QY 1213 ATATTGATAGATTTCAAGTTTGAAGTTAAGTGTGCTGATTTGCTTGTGTAAGATGCT 1272
DB 874 ATTTGCTTGTATGCTCAATGGAATGCTAAGGTATCAGATTTTGGACTTGTAGCTTTG 933
QY 1273 CTGATACAAACAGCATGATATCAACACGTGTGATGGAACCTTTGGTACTTGGCTCCG 1332
DB 934 TCTCCGAGAGCAGCTACGTGACAACCCGAGTAATGGAACCTTTTGGATATGTTGGCCT 993
QY 1333 GAATAGCTCCAGCGGAAGCTCACGGAGAAGTCTGACGCTTTCTCATTTGGCTGTG 1392
DB 994 GAGTATGCTTGCACCGGAATGTTGACAGAAAAGATGATATCATAGTTTGGGATATTA 1053
QY 1393 CTTTGGAGCTATTACTGGACGCTGACCCGTTGATGCCAACAAATGCTATGATGATGAC 1452

DB 1054 ATCATGGAGATAATCACCGGAGAAATCTCTGCAATTAATAGTCACCTCAGGAGGTG 1113
QY 1453 AGCTTAGTTGACTGGGACAGCACTTCTT---AACCGAGCATCTGACCAAGAGAC 1506
DB 1114 AATTTGGTTGAGTGCTTGAAACAAATGTTGAAACCGAAGTCTCTGAGGAAGTAGTC 1170

RESULT 14
US-09-887-576-179/c
; Sequence 179, Application US/09887576
; Patent No. US20020144047A1
; GENERAL INFORMATION:
; APPLICANT: Budworth, P.
; APPLICANT: Brown, D.
; APPLICANT: Chang, H.
; APPLICANT: Zhu, T.
; APPLICANT: Han, B.
; APPLICANT: Wang, X.
; APPLICANT: Cooper, Bret
; TITLE OF INVENTION: Promoters for regulation of plant expression
; FILE REFERENCE: 1360.001US1
; CURRENT APPLICATION NUMBER: US/09/887,576
; CURRENT FILING DATE: 2001-06-25
; PRIOR APPLICATION NUMBER: US 60/213,848
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: US 60/214,087
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: US 60/258,692
; PRIOR FILING DATE: 2000-12-29
; NUMBER OF SEQ ID NOS: 875
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 179
; LENGTH: 2004
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-887-576-179

Query Match 10.0%; Score 194.8; DB 10; Length 2004;
Best Local Similarity 55.5%; Pred. No. 6.6e-46;
Matches 401; Conservative 0; Mismatches 312; Indels 9; Gaps 1;

QY 799 GAGCTAGCTAGAGCCACCACATGTTCTCCGAGGCGAACTTGTAGACAAAGCGGGTTC 858
DB 991 GAGCTTGAAGTTCCTACTAATGGAATTCCTGACGAGAATGATTTGACAGAGAGGTAT 932
QY 859 GGTACGTCGCAAAAGGTGTGTGCTAGTGGGAAGAAGTGTGCTGTAAGACAGTTGAAA 918
DB 931 GGGATTTGTATAGAGTGTCTTTGAGGATAAATCAATGGTGGCTATAAGAATCTGCTC 872
QY 919 GTTGGAGTGTGCGAGGAGAGAGGAGTTTCAGGACAGAGTGTAGATCATCAGCAGAGTT 978
DB 871 AACACAGAGGACAGCTGAGAGAAGAAATTAAGTCGAAGTCGAAGCTATTGGAGCCGTA 812
QY 979 CACCACAGGCATCTGCTCTCTTGTGTTATTCATCGCGGTGCCAAAAGATTGCTT 1038
DB 811 AGACACAGATCTGTTGAGATGCTTGTGTTATTCGTTGAGAGAGCTCATAGGATGTA 752
QY 1039 GTCATAGATTGTTTCCCTAACAAATCTCGAGCTTCACCTCCATGCGGAGGG----- 1091
DB 751 GTTTACGAGTATGTTGATAATGGGAATTTAGAACAAATGGAATTCATGTTGGTGTGGG 692
QY 1092 --ACGGCTACAAATGGATGGAGCAGCAGATTTGAAGATTTGCTTGGATCTCTAAAGTA 1149
DB 691 TTTAAGAGTCTCTTACTTGGAGATTAGGATGACATTTGTTTGGACAGCCAAAGGG 632
QY 1150 CTCTTCTTATCTTCATGAAGATTCGAATCTTAAATCATTCACCGTATCAAGGCTTCA 1209
DB 631 TTAATGATTTTACAGAGAGGCTTTGAGCCTTAAGTGTGTTACCGAGATTTAAATCGAGT 572
QY 1210 AACATATTGATAGATTTTCAAGTTTGAAGTAAAGTGTGCTGATTTTGGCTTTGCTAAGAT 1269
DB 571 AATATCTGTTGACAGCAATGGNACTCGAAGTCTTCTGACTTTGGGTAGTAGCTC 512

| | | | |
|----|------|---|------|
| QY | 1270 | GCTTCTGATACAAACACGCATGTATCAACACGCTGTGATGGAAACCTTTGGGTACTTGGCT | 1329 |
| Db | 511 | TTGGSTTCGGAGATGACCTATGTGTCACCTACCTCCTGTGATGGTACGTTTGGGTATGTGGCT | 452 |
| QY | 1330 | CCGGAATACGCTGCAACCGGAAGAGCTCACGGAGAAGTCTCAGCTTTTTCATTTGGCGGTT | 1389 |
| Db | 451 | CCTGAATACCGAGTACCGGAATGTGAATGAGAGGACGATGTTTATAGCTTCGGTGTT | 392 |
| QY | 1390 | GTGCTTTTGAGAGCTCATTTCTGGACGTCGACCCGTTGATGCCAACAACTCTATGTAGAT | 1449 |
| Db | 391 | CTTCTTTATGAGATTATTTTCAGGAGAGTCTCTGTGGAATTATACCGCGGCTCCGGAGAA | 332 |
| QY | 1450 | GACAGCTTAGTTGACTGGGACAGACCATTTGCTTTAACCGAGCATCTGAGCAAGGAGACTTT | 1509 |
| Db | 331 | GTGAATCTTTGGAATGGTTTGAAGAGATTGTCGCGAATCGATGCGGAAGGAGTTTG | 272 |
| QY | 1510 | GA 1511 | |
| Db | 271 | GA 270 | |

RESULT 15

US-36-938-842A-1079
; Sequence 1079, Application US/09938842A
; Patent No. US20020160378A1
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeff
; APPLICANT: Kreps, Joel
; APPLICANT: Wang, Xun
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: SAME, AND METHODS OF USE
; FILE REFERENCE: SCRIPT300-3
; CURRENT APPLICATION NUMBER: US/09/938,842A
; CURRENT FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/227,366
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/264,647
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/300,111
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO 1079
; LENGTH: 2124
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-938-842A-1079

[illegible]

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| QY | 1080 | CCATGG-----CGAGGACGGCCTCAATGGGAATGAGCACCGAGATTGAAGATTGCTCT | 1133 |
| Db | 1347 | CCATGGGCCTCTCGGGTTGAACCTGCTCTTGATTGGGACCCAGAAATGAAGATTGCAC | 1406 |
| QY | 1134 | TGGATCTGCTAAAGGAGCTTCTTATCTTCATGAGATTGCAATCCCTAAATCATTTCAACG | 1193 |
| Db | 1407 | TGATGCTGCAGAGAGACTTGATACCTTTCATGAAGACTCGCAACCCCTCCGTTATACACAG | 1466 |
| QY | 1194 | TGATATCAAGGCTTCAACACATATTGATAGATTTCAGTTTGAAGCTAAGGTGCTGATTT | 1253 |
| Db | 1467 | AGATTTTAAAGCCTCTAATATATCTCTTGAACAACTTCAAGCCCAAGTTGCGATTT | 1526 |
| QY | 1254 | TGGTCTTGGCTAAGATTCCTTCTGATACAA---ACGCGATGTATCAACAGTGTGATGGG | 1310 |
| Db | 1527 | TGGCCTAGCCAAACAAAGCTCCTGAAGCAGGGGTAACTCACTTATCTACTCGTCTTATGGG | 1586 |
| QY | 1311 | AACCTTTGGCTACTTTGGCTCTCGGAAATACGCTSCAAGCGGAAGACTCAGGAGAGATCTGA | 1370 |
| Db | 1587 | CACATTTGGATATGTTGGCGCTGAATATGCAATGACGGGACACCTACTCGTCAAGATGA | 1646 |
| QY | 1371 | CGTTTTCCTAATTTGGCGCTTGCTTTTGGAGCTCAATTACTGGACGTCGACCCGTTGATGC | 1430 |
| Db | 1647 | TGTTTATAGTACGGTGTGTCCTCTCGAATTCCTTAACTGGTAGAAGACCTGTGAGTAT | 1706 |
| QY | 1431 | CACAAATGCTATGTAGATGACAGCTTAGTTGACTGGGCACGACCAATTCCTTAACGAGC | 1490 |
| Db | 1707 | GTCAACACCTTCAGGCCCCAGAAAATCGTCACTTGGACAAGGCCAGTCTT----- | 1757 |
| QY | 1491 | ATCTGAGCAGGAGACTTTGAGGGTTTAGCTGATGCAAGATGAATAATGGGTTTGCACAG | 1550 |
| Db | 1758 | AAGAGCAAGACCGGTTAGAAAGATAGTCGGAATCAAGACTTGAAGGAAAAATACCCGAA | 1817 |
| QY | 1551 | AGAGGAGATGGCTCGCATGGTTGCTTGCTGGGCTTGTTGTGGCATTCACCTCGCCG | 1610 |
| Db | 1818 | AGAGATTTTCATAAGAGATGCAACAATCGCTGAGCTTGTGTGCCACTGAAGCTAGCCA | 1877 |
| QY | 1611 | CAGACCTCGGATGAGCGGATTTGGC | 1636 |
| Db | 1878 | GGACCAACAGATGGGGAAGTGGTTC | 1903 |

Search completed: July 7, 2003, 08:04:54
Job time : 341 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compendex Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 7, 2003, 07:29:23 ; Search time 2356 Seconds

(without alignments)
11023.819 Million cell updates/sec

Title: US-10-086-464-1

Perfect score: 1944

Sequence: 1 atgtctctggcgccgtctcc.....atagtgacctctctttaa 1944

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 16154066 segs, 3097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*

1: em_estba:*
2: em_esthum:*
3: em_estnu:*
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5: em_estnu:*
6: em_estpl:*
7: em_estro:*
8: em_hic:*
9: gb_est1:*
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15: em_estfun:*
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18: em_gss_hum:*
19: em_gss_inv:*
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23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
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27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----|--------------------|
| 1 | 442.2 | 22.7 | 759 | 13 | BM408099 EST582426 |
| 2 | 429.6 | 22.1 | 757 | 12 | BG596561 EST495239 |
| 3 | 413.2 | 21.3 | 692 | 12 | BG441204 GA_Pa001 |
| 4 | 411.6 | 21.2 | 584 | 10 | AV543493 AV543493 |
| 5 | 400 | 20.6 | 666 | 13 | BM358715 GA_Pa001 |
| 6 | 399 | 20.5 | 573 | 10 | AV551753 AV551753 |

| | | | | | | |
|----|-------|------|------|----|----------|-----------|
| 7 | 376 | 19.3 | 1053 | 11 | AY108241 | Zea mays |
| 8 | 366.2 | 18.8 | 1016 | 11 | AY108243 | Zea mays |
| 9 | 358.4 | 18.4 | 645 | 14 | BQ506869 | EST614284 |
| 10 | 356.2 | 18.3 | 652 | 14 | BQ849683 | QGB10120 |
| 11 | 349.2 | 18.0 | 593 | 12 | BF176907 | EM1_4_B10 |
| 12 | 348.6 | 17.9 | 646 | 14 | BQ240617 | TaF05015B |
| 13 | 348.2 | 17.9 | 537 | 14 | BQ134241 | BQ134241 |
| 14 | 345.8 | 17.8 | 679 | 14 | BQ404121 | GA_Pd006 |
| 15 | 337.2 | 17.3 | 770 | 14 | BQ999193 | QGG31G04 |
| 16 | 336.2 | 17.3 | 631 | 10 | BE330924 | SO9B0C1.Y |
| 17 | 332 | 17.1 | 933 | 10 | AK982539 | HVSMF9000 |
| 18 | 329.6 | 17.0 | 718 | 13 | BM407268 | EST581595 |
| 19 | 322.6 | 16.6 | 673 | 14 | BQ410602 | BM407268 |
| 20 | 320.4 | 16.5 | 608 | 14 | BM814985 | GA_Pd003 |
| 21 | 316.8 | 16.3 | 561 | 10 | AV539333 | AV539333 |
| 22 | 315.2 | 16.2 | 643 | 12 | BF202789 | WHE1784.F |
| 23 | 315 | 16.2 | 548 | 13 | BM527398 | sal61d03 |
| 24 | 308 | 15.8 | 593 | 14 | BQ850206 | QGB11P07 |
| 25 | 307.8 | 15.8 | 578 | 10 | AV917322 | AV917322 |
| 26 | 303.2 | 15.6 | 625 | 14 | BM878778 | P16-C03.S |
| 27 | 300.2 | 15.4 | 548 | 9 | AI728857 | BNLGH1118 |
| 28 | 299.4 | 15.4 | 484 | 12 | BG817458 | EM1_76_C0 |
| 29 | 299.2 | 15.4 | 573 | 14 | BM815391 | EST593485 |
| 30 | 298.4 | 15.3 | 497 | 12 | BF201900 | WHE1759-1 |
| 31 | 296 | 15.2 | 546 | 12 | BG511034 | sac65a03 |
| 32 | 295.4 | 15.2 | 529 | 10 | BE637850 | WHE1755-1 |
| 33 | 295 | 15.2 | 525 | 12 | BG448469 | BF036E04R |
| 34 | 284.6 | 14.6 | 735 | 14 | BQ788651 | WHE4152_C |
| 35 | 283.4 | 14.6 | 453 | 17 | BH442220 | ROGLN68TR |
| 36 | 280.4 | 14.4 | 502 | 12 | BG369831 | HVSMF1002 |
| 37 | 280.2 | 14.4 | 672 | 14 | BQ005676 | QGG8M18.Y |
| 38 | 273.6 | 14.1 | 459 | 10 | AV538962 | AV538962 |
| 39 | 266.2 | 13.7 | 720 | 13 | FC283891 | BJ283891 |
| 40 | 265.6 | 13.7 | 544 | 10 | BE492937 | WHE0563_B |
| 41 | 258.6 | 13.3 | 489 | 10 | AW982145 | SS00075.S |
| 42 | 256 | 13.2 | 628 | 10 | AV826238 | AV826238 |
| 43 | 255.6 | 13.1 | 618 | 10 | AV826648 | AV826648 |
| 44 | 254.4 | 13.1 | 610 | 13 | BJ305865 | BJ305865 |
| 45 | 253.6 | 13.0 | 436 | 10 | AV793009 | AV793009 |

ALIGNMENTS

RESULT 1
BM408099
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
FEATURES

BM408099
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end, mRNA sequence.
BM408099
BM408099.1 GI:18259729
EST.
potato.
Solanum tuberosum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
1 (bases 1 to 759)
van der Hoeven, R., Sun, H., Karamycheva, S.A., Tsai, J., Van Aken, S.,
Tattersall, T., Chieming, A., Bougri, O., Buehl, C.R., Rooning, C.,
Tanksley, S. and Baker, B.
Generation of ESTs from potato roots
Unpublished (2001)
Contact: Research Genetics, Libraries Division
Tel: 1-800-711-6195
Email: cdna@resgen.com
For clone info: please contact Research Genetics, Libraries
Division tel 1-800-711-6195, email cdna@resgen.com
Seq primer: T3.
Location/Qualifiers
1..759
/organism="Solanum tuberosum"
/cultivar="Kennebec"


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FEATURES source
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1. 584
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XhoI"
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Best Local Similarity 90.9%; Pred. No. 3.3e-88;
Matches 438; Conservative 0; Mismatches 44; Indels 0; Gaps 0;
QY 1463 ACTGGCAGCACCATTGCTTACCGAGCATCTGACCAAGGAGACTTTGAGGTTAGCTG 1522
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
584 ACTGGCAGCACCATTGCTTACCGAGCATCTGAGGAAGGAGATTGAGGGTTGGCTG 525
QY 1523 ATCAAGATGAATATGGGTATGACAGAGGAGATGGCTCGCATGAGCCAGATGATGCGCTG 1582
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
524 ATCAAGATGAGTATGATGATGACAGAGGAGATGGCTCGCATGAGTTGCTGCGCTG 465
QY 1583 CGGCTGTGTCGCCATTCAGCTCGCCGACACCTCGCATGAGCCAGATTTGCGTGCCT 1642
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
464 CGGCTGTGTCGCCATTCAGCTCGCCGACACCTCGCATGAGCCAGATGATGCGGCT 405
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344 TATACAGCTCATATGAGGAGCAGCAGATATGACACGAGCCATACACGACGACATGA 285
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284 TAAAGTTAGAAAATGCTTGGACATCAAGTAGTACGCCAGCAGCAGGCTGAGTACAGTA 225
QY 1823 ATCCGACAGTGACTATGACTGTACCGCTTGGTTCAAGCAGCGAGGCCAAGCAGAC 1882
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Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
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Db ||
104 AA 103
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BM358715
LOCUS
DEFINITION BM358715 666 bp mRNA linear EST 09-JAN-2002
Gossypium arboreum 7-10 dpa fiber library Gossypium
ARBOREUM cDNA clone GA_Ea0012D16r, mRNA sequence.
ACCESSION BM358715
VERSION BM358715.1 GI:18099461
KEYWORDS EST.
SOURCE
ORGANISM Gossypium arboreum.
Gossypium arboreum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Malvales; Malvaceae; Gossypium.
REFERENCE 1 (bases 1 to 666)
Wing, R.A., Frisch, D., Yu, Y., Main, D., Rambo, T., Simmons, J., Henry
D., Wood, R.C., Leslie, A. and Wilkins, T.A.
An integrated analysis of the genetics, development, and evolution
of the cotton fiber
Unpublished (2003)
```

COMMENT

Contact: Wing RA
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
Email: rwing@clemson.edu
Total High Quality bases = 646
Seq primer: TAATAGACTCTACTATAGG
High quality sequence stop: 666.
Location/Qualifiers

FEATURES source

1. 666
/organism="Gossypium arboreum"
/strain="AKA"
/cultivar="8400"
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/tissue_type="Fibers isolated from bolls harvested 7-10
dpa"
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BASE COUNT 178 a 134 c 167 g 187 t
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Best Local Similarity 75.6%; Pred. No. 2.1e-85;
Matches 496; Conservative 0; Mismatches 160; Indels 0; Gaps 0;

QY 739 CTCTCCACCGTCTCCAGGGCTTGTGTAGGCTTCTCCAAAAGCACITTCACATACGAG 798
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11 CTTCGGCTCCCTGCTACCTGTATTTCTTAGGTTTCGAAAAGCACITTTAGCTATGAA 70
QY 799 GAGTAGCTAGAGCACCACCAATGTTTCTCGAGGCGCACTTGTAGGACAGCCGCTTC 858
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
71 GAATTAGCAGAGCAACGATGCTTCTCGAAGTTAACTCTTGGCAAGGTGTTTT 130
QY 859 GGTTCAGTGCACAAAGGTGTGTTCCTAGTGGGAAAGAGTTCCTGTAAGCAGTTGAAA 918
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
131 GGGTAGCTACACAAAGGAGTTCCTCCTAATGGAGAGTAGCAGCAAGCACTCAAG 190
QY 919 GTTGGAGTGTTCAGGAGAGAGGAGTTTCAGGAGAGGTGAGATCATCAGCAGAGTT 978
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
191 GCTGGAAGTGGGAGGAGAGAGAAATTCAGGCTGAAGTTGAGATCATTAGCCGCTC 250
QY 979 CACCACAGCACTCGTGTCTCTTGTGTTATTCATCGCCGCTGCCAAGAGATGCTT 1038
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251 CATCAACACCTCTGCTCTCAITGGTGGATCTGTTTCTGGGACAAATAGAAATGCTT 310
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311 GTTATGAGTTTCTCAACCAACACCTTCGAGTTTCACTTCATGGGAGGAGGAGCTG 370
QY 1099 ACAATGGAATGGAGCACCAGATGAAGATGCTCTTGGATCTGCTAAGAGACTTCTTAT 1158
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371 ACCATGGATGGCCAGCAGGATGAAATTTGTTAGGATCTSCAAAAGGACTTGGCATAT 430
QY 1159 CTTCATGAAGATTGCAATCTAAATCATTCACCGTGATATCAGGCTTCAACATATG 1218
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431 CTTCATGAAGATTGTCATCTAAGATCATTCACCGTGATATTAAGCCCTCTATATCTG 490
QY 1219 ATAGATTTCAAGTTTGAAGCTAAGTTGCTGATTTTGGTCTTCTTAAGATGCTTCTGAT 1278
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491 TTGGATTTCAAGTTTGAAGCAAAAGCTTCTGATTTTGGACTAGCGAAAATGCTTCCGAT 550
QY 1279 ACAACACGATGATACACAGCTGTGATGGGAACCTTTGGTACTTGGCTCGGAATAC 1338
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
551 GTCACAGCGAGCTCTCCACAGGCTGATGGGTACTTTTCGGGTATTTAGCCCTCAGTAT 610
QY 1339 GCTGCAAGCGGAAAGCTCACGAGAGTCTGACGTTTCTCATTTGGCTTCTGCT 1394
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611 GCTTCAGTGGAAAGCTCCTGATATATCAGATGTTTCTCTCTCTCGGGTCTATGCT 666

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RESULT 6
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LOCUS             Arabidopsis thaliana roots Columbia Arabidopsis thaliana
DEFINITION        cDNA clone RZ13C07R 5', mRNA sequence.
ACCESSION         AV551753
VERSION           AV551753.1 GI:8723166
KEYWORDS          EST.
SOURCE            thale cress.
ORGANISM          Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eustoids II; Brassicales; Brassicaceae; Arabidopsids.
1 (bases 1 to 573)
Asamizu E., Nakamura, Y., Sato, S. and Tabata, S.
A large scale analysis of cDNA in Arabidopsis thaliana: Generation
of 12,028 non-redundant expressed sequence tags from normalized and
size-selected cDNA libraries
DNA Res. 7, 175-180 (2000)
20363093
Contact: Erika Asamizu
The First Laboratory for Plant Gene Research
Kazusa DNA Research Institute
Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
Email: asamizu@kazusa.or.jp, URL: http://www.kazusa.or.jp/en/plant/.
Location/Qualifiers
1. 573
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XhoI"
BASE COUNT      147 a 132 c 139 g 155 t
ORIGIN
Query Match      20.5%; Score 399; DB 10; Length 573;
Best Local Similarity 83.6%; Pred. No. 3.5e-85;
Matches 473; Conservative 0; Mismatches 85; Indels 9; Gaps 2;

QY 419 TGGAAATCGCATCGGAGAGTCGCTGCTGTGTGATGAGTACGCTGATGCTCTCT 478
Db 1 TAGAAATCGCATCGGAGAGTCGCTGCTGTGTGATGAGTACGCTGATGCTCTCT 60

QY 479 GTAGGAAGAACACGCGGAGA-----GACGAAGAAGATGCTTACTATGTTCCCTCCGAC 532
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QY 533 CTCCTCTGCTCCCAAGCCGAGGACCTTACGGTGACAGACACATGCGGCAAC 592
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QY 593 AAAACGCAACACACCGCTCAGATCATGTGCTGACGTCACTACCAACACCACTAAGGCTC 652
Db 181 AAAACGCGTCACGCGCTCAGATAATCATGTAGTACGTCTATGCGCACCACTAAGGCTC 240

QY 653 CATCTCCACACCGGCAACCTCCCT---CCACCTCCACCGCCCTTTCATGAGCAGCAGCG 709
Db 241 CATCTCCACACCGGCAACCTCCCTCCGCACTCCACCAACGAGCATTCATGAGTAGCAGTG 300

QY 710 GCGGCTCCGACTACTCGGACCGTCCAGTCTTCTCCACCGTCTCCAGGCGGTGTTAG 769
Db 301 GTGGTCTGACTATTGCGATCTTCCGGTTCTTCTCCACCATCTCCAGGCGGTGTTAG 360

QY 770 GCTTCTCCAAAAGCACTTTCATACAGGAGGAGTAGCTAGACACCAATGTTCTCCG 829
Db 361 GCTTCTTAAGACACTTTCATATGAGGAGTGTGCGAGAGTACTAATGGGCTTCTCTG 420

QY 830 AGCGCACTTGTAGGACAAAGCGGGTTCCGTTACGTGCACAAAGGTGTGTGCTAGTG 889

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Db 421 AGGCTAATTTGTTAGGACAAGAGGGGTTGGTTATGTGCAATAAAGTATATATGCGCTAGTG 480
QY 890 GGAAGAAGTTGCTGTGAAGCAGTTTAAAGTTGGAGTGGTCAGGAGAGAGGAGTTTC 949
Db 481 GGAAGAAGTTGCTGTGAAGCAGTTTAAAGTTGGAGTGGTCAGGAGAGAGAGTTC 540
QY 950 AGGCAGAGTTGAGATCATCATCAGCAGTTCACC 982
Db 541 AGGCTGAGTTGAGATCATCATCAGCAGTTCATC 573

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LOCUS             Zea mays PCO134818 mRNA sequence.
DEFINITION        Zea mays PCO134818 mRNA sequence.
ACCESSION         AY108241
VERSION           AY108241.1 GI:21211319
KEYWORDS          HTC.
SOURCE            Zea mays.
ORGANISM          Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 1053)
Hainey, C.F., Dolan, M., Miao, G.H., Vogel, J.M., Whitsitt, M.S.,
Arthur, L.W., Hanafey, M., Morgante, M. and Tingey, S.V.
Maize Mapping Project/DuPont Consensus Sequences for Design of
Overgo Probes
Unpublished (2002)
2 (bases 1 to 1053)
Coe, E.C.
Direct Submission
Submitted (25-APR-2002) Maize Mapping Project, University of
Missouri, Columbia, MO 65211, USA
Location/Qualifiers
1. 1053
/organism="Zea mays"
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Library"
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assemblies resulting from the application of public
contigs to seed DuPont contigs; this resource was
assembled by DuPont as part of a collaboration for the
overgo addressing of BAGs in conjunction with the Maize
Mapping Project"
BASE COUNT      283 a 220 c 262 g 288 t
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Query Match      19.3%; Score 376; DB 11; Length 1053;
Best Local Similarity 68.5%; Pred. No. 1.5e-79;
Matches 566; Conservative 0; Mismatches 250; Indels 10; Gaps 3;

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Db 11 GGAATGAGCAGCAGATGAGATGCTCTTGGAT-CTGCTAAGAGCTTCTTATCTTC 70

QY 1163 ATGAAGATTGCAATCTTAAATCATTCACCGTGATATCAAGGCTTCAAAACATATTGATAG 1222
Db 71 ATGAAGACTGCCATCCCAAGATCATCATCTGATATAAGGATCATCAATCTTCTTG 130

QY 1223 ATTTCAAGTTGAGCTAAGGTTGCTGATTTGGTCTTGTGCTTAAGATGCTTCTGATACAA 1282
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QY 1283 ACAGCATGATCAACACGCTGTGATGGGAACCTTTGGTACTTGGCTCGGAAATACGCTG 1342
Db 191 ACACCCATGTTTCGACAAAGAGTAATGGCACCTTTGGGTATTTGGCACCTGAGTAGCAT 250

QY 1343 CAAGCGGAAGCTCACGGAGAGTCTGACGTTTCTCATTTTGGCTTGTGCTTTGGAGC 1402

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Db      251 CTCTGGCAAGCTACAGAAATCGATGTAATTTCTCTCGAGTCATGCTCTTGAGC 310
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Db      311 TTATTACTGGGGCGGCGACAGCTTGACAAACCAACCAATATATGATGACAGCTTGGTGG 370
QY      1463 ACTGGGCAAGCACTGCTTAACCGAGCATCTGACCAAGGAGACTTTGAGGTGTAGCTG 1522
Db      371 ACTGGGCAAGGCACTTACTGATGCGAGCAGCTTGAGGATGGTGAATATGATGCTTATGG 430
QY      1523 ATGCAAGAAATGATATGGGTATGACAGAGAGAGATGGCTCGCATGTTGCTGCTGCTG 1582
Db      431 ATCTCTGCGCTGGGAAGGACCTCAATCTATAGATGCGAGAGATGATGATGCTGTGCGAG 490
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Db      491 CTGCTGTGTAGCCCATCTGCACTGCGAGCAGCTGCGGCCACGTATGATGCTGCGGCTT 550
QY      1643 TAGAAGGAATGATCACTGTGAGATCTTAACGAGGAGATGAGCAGGCTCAAGCAATG 1702
Db      551 TGGAGGCAATGTCTTTGGAGGACCTTAATGAGGTGTTGGGCTGCGCCATAGCCGCT 610
QY      1703 TATACGCTATACGGGAAGACCGGATTTATGACTCGAGCCAGTACAAATGAAGACATGA 1762
Db      611 TCTTTGGGTATAC---AGCAGCTCCGATTCAGATTTCTGCGCCAGTACACGAGGCATGA 667
QY      1763 AGRAGTTAGAAATGGCACTTGAGCTTGAAGTCAAGAGTACAAAGCCGAGGCTGAGTACAGTA 1822
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Db      722 CGCCAAACAGTGAATATGGACAGATACGCTTCTGATCAGCAGGAGGCGCCACAGCAGC 781
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RESULT 8
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LOCUS      Zea mays PC0134814 mRNA linear HTC 25-MAY-2002
DEFINITION Zea mays PC0134814 mRNA sequence.
ACCESSION AV108243
VERSION    AV108243.1 GI:21211321
KEYWORDS   HTC.
SOURCE     Zea mays.
ORGANISM   Zea mays
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
            clade; Panicoideae; Andropogoneae; Zea.
REFERENCE  1 (bases 1 to 1016)
            Hainey,C.F., Dolan,M., Miao,G.H., Vogel,J.M., Whitsitt,M.S.,
            Arthur,L.W., Hanafey,M., Morgante,M. and Tingey,S.V.
            Maize Mapping Project/DuPont Consensus Sequences for Design of
            Overgo Probes
            Unpublished (2002)
REFERENCE  2 (bases 1 to 1016)
            Coe,E.C.
            Direct Submission
            Submitted (25-APR-2002) Maize Mapping Project, University of
            Missouri, Columbia, MO 65211, USA
FEATURES   Location/Qualifiers
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                /note="this sequence is part of a project of EST
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assembled by DuPont as part of a collaboration for the
overgo addressing of BACs in conjunction with the Maize
Mapping Project"
BASE COUNT 261 a 231 c 262 g 262 t
ORIGIN

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Query Match      18.8%; Score 366.2; DB 11; Length 1016;
Best Local Similarity 68.7%; Pred. No. 3.3e-77;
Matches 535; Conservative 0; Mismatches 238; Indels 6; Gaps 2;

QY      1115 CCAGATTGAGATTCCTCTTGGATCTGCTTAAAGGACTTCTTATCTTCATGAAGATGCA 1174
Db      1 CTAGATTAAGATCGCTCTGGGTGCTGCCAAGGTTTAGCTTATCTTCATGAAGACTGCC 60
QY      1175 ATCCCTAATATCATTCACCGTGATATCAAGCTTCAACATATATGATGATTCAGTTTG 1234
Db      61 ATCCAAAGATCATCCACCGGACATTAAGGCATCTAATCTCTCTTGTGACTTCAAAATTG 120
QY      1235 AAGCTAAGGTTGCTGATTTTGTCTTAAAGATTCCTTGTATACAAACACCATGTAT 1294
Db      121 AAGCTATGTTGCTGACTTTGGACTTGCAGAGTTCTACTACTGATACACACCCATGTGT 180
QY      1295 CAACAGGTGTGATGGGAACCTTTGGTACTTGGCTCCGGAATACGCTCAAGCGGAAGC 1354
Db      181 CAACAAGAGTAAATGGGACCTTTGGTATTTGGCAACCGAGTATGCAAGCATCTGGCAAGC 240
QY      1355 TCACGGAGAAGTCTGACGTTTTTCATTTGGCGTTGTGCTTTTGGAGCTCATCTAGGAC 1414
Db      241 TCACAGAAATTCAGATGATTTTCTTCGGAGTATGCTTCTTGAGCTTATTTACTGGGC 300
QY      1415 GTGACCGGTTGATGCCAACAATGTCTATGTAGTATGACAGCTTAGTTGACTGGGCACGAC 1474
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QY      1475 CATTCCTTAACCGAGCATCTGAGCAAGGAGACTTTCAGGCTTTAGCTGATGCAAGATGA 1534
Db      361 CATTAAGTATGAGAGCGCTCGAGGATGTTGAATATGATGCTTGTGGATCTCGGCTCG 420
QY      1535 ATAATGGTATGACAGAGAGAGATGGCTCGCATGTTGCTGTGCTGGCTTGTGTTC 1594
Db      421 GAAAGGACTTCAATCTTAACGAGATGSCAAGANTGATAGCTGTGCGCTGCTGCGCTAC 480
QY      1595 GCCATTAGCTCGCGGAGACCTTCGCATGAGCCAGATTTGCGTTCGCTTAGAAGAAATG 1654
Db      481 GCCATTCCGACGCTGCTCGGCACGAATGATGATGATGCTGCTGCGGCTCTGGAAGCGCAG 540
QY      1655 TATCACTGTCAGATCTTAACGAAGGATGAGACCGAGTCAAGCAATGTATACACTCAT 1714
Db      541 TGTCTTTGGAGACCTTATGAGGTGTTTCGACCTGGCCATAGCCGCTTCTTTGGGTGAT 600
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QY      1835 ACTATGCACTGTACCGCTTGGTTCAAGCAGGAGGCGCAACCAACACGCGCAATGAG 1893
Db      715 AATACGCCAGGTGCGCTCTGGATCAAGCAGGAGGCGCGCCGACGAGGAGATGGAG 773

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RESULT 9
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LOCUS      BQ506869
DEFINITION EST614284 Generation of a set of potato cDNA clones for microarray
            analyses mixed potato tissues Solanum tuberosum cDNA clone STMGM90
            5' end, mRNA sequence.
ACCESSION BQ506869
VERSION    BQ506869.2 GI:21922719
KEYWORDS   EST.
SOURCE     potato.

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ORGANISM Solanum tuberosum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
REFERENCE 1 (bases 1 to 645)
AUTHORS Buell, C.R., Hart, A., Baker, B., Tanksley, S., Fry, W., Smart, C.,
Restrepo, S., Griffiths, H., van der Hoeven, R., Tsai, J., and
Karyancheva, S.A.
TITLE Generation of a set of potato cDNA clones for microarray analyses
JOURNAL Unpublished (2002)
COMMENT On Jun 10, 2002 this sequence version replaced gi:21365738.
Other ESTs: EST614285
Contact: Robin Buell
The Institute for Genomic Research
9712 Medical Center Dr, Rockville, MD 20850, USA
Email: potato@tigr.org
This clone is available through the Research Genetics, contact the
Research Genetics for further information 1-800-711-6195 or
cda@resgen.com
Seq primer: T3.
FEATURES
source Location/Qualifiers
1..645
/organism="Solanum tuberosum"
/cultivar="Kennebec or Binjete"
/db_xref="taxon:4113"
/clone="STM3430"
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/note="Vector: pBluescript SK(-); Site 1: EcoRI; Site 2:
XhoI; supplier: Combination of untreated and Phytophthora
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axillary buds of stem explants, petioles, germinating eyes
, tubers, or roots."
BASE COUNT 175 a 124 c 154 g 192 t
ORIGIN
Query Match 18.4%; Score 358.4; DB 14; Length 645;
Best Local Similarity 74.3%; Pred. No. 2.1e-75;
Matches 452; Conservative 0; Mismatches 156; Indels 0; Gaps 0;
QY 901 GCTGTGAAGCAGTGGAAAGTTGGGAGTGTGTCAGGAGAGAGAGGAGTTTCAGGACGAGTT 960
DB 1 GCAGTTAAACAGCTTAAGCTTGGAGTGGAGAGAGGAGAGGAGTTTCAGGCGGAGATT 60
QY 961 GAGATCATCAGCAGAGTTTCACACAGGCACTGTGTCTCTGTGTGGTATTCGATCGCC 1020
DB 61 GAGATTATTAGCGGATACATCACAGCACTGTGTCTCTGTGTGGATCTGCATTACT 120
QY 1021 GTGCGCAAGATTCGTTGTATGAGTTTGTCTTACACACAACTCGAGCTTCACCTC 1080
DB 21 GGGCTCAGAGACTGCTTGTATGAGTTTGTCTTACCAACAACTTCGAAATTCATTATTA 180
QY 1081 CATGGCAGGAGCGGCTACAAATGGAATGGAGCAGACAGATTGCAAGATTGCTTGGATCT 1140
DB 181 CACGGAAGGAGGAGCCCTCTTGGATTGGCCATACGCTAAAGATTGCTCAGGATCA 240
QY 1141 GCTAAGAGACTTTCTATCTCATGAGCAATTCGAATCCTAAATCAATTCACCGTATATC 1200
DB 241 GCTAAGAGACTGGCATATCTGATGAGACTGCCAACCGAAATCATTCACCGTATATC 300
QY 1201 AAGCTTCAACATATTGATAGATTTCAGTTTGAAGTTGAAGTTGCTGATTTTGGTCTT 1260
DB 301 AAGCAGCATTAATTAATCTATGACTTTAATTTGAGGCTTAAGTTGCTGATTTGGACTT 360
QY 1261 GCTAAGATTGCTTCTGATAAACAACGCGATGATCAACAGCTGTGATGGAGACCTTTGGG 1320
DB 361 GCCAAGTAACTCTGATGTTTAATTAATCTATGCTTCCACAGAGTGTGGAACCTTTGGG 420
QY 1321 TACTTGGCTCCGATACGCTGCAAGCGGAAAGCTTCACGGAGAGTCTGACGTTTTCTCA 1380
DB 421 TATTGGCTCCAGATATGCTTCTCTGGAAGCTTACAGACAACTCAGACGATATCTCC 480

QY 1381 TTGGCGTGTGCTTTGGAGCTCATTTACTGAGCTGACCGCTTGAICCCACAAATGTC 1440
DB 481 TTGGTGAATGCTTTTGAAGTTGATTAAGTGAAGCTGCGCTTGTGACTCTACTCAATCA 540
QY 1441 TATGTAGATGACAGCTTACTTACTGCTGGGACACGACATTCCTTAACCGAGCATCTGAGCAA 1500
DB 541 TCATCTGAGATAGTTTGTGGACTGGGACGCTCCATTAATCTACAGGAGCTTTAGAAGAT 600
QY 1501 GGAGACTT 1508
DB 601 GAAAGTTT 608

RESULT 10
BQ849683

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

Location/Qualifiers

1..652

/organism="Lactuca sativa"

/cultivar="Salinas"

/db_xref="taxon:4236"

/clone="QGB10120"

/lab_host="E.Coli"

/note="Vector: pBRCDNASFIAB; The library was constructed

from 10 different sources of RNA from a single genotype.

Separate cDNAs were generated using primers that

incorporated unique 5' and 3' tags to distinguish each

source of RNA. cDNAs were then pooled, size-fractionated,

directionally cloned into a custom medium-copy vector and

transformations made with four size classes to minimize

size bias. Details of each source of RNA and library

construction can be obtained at http://cgdb.ucdavis.edu/

YAG_LIB=QGB10120

YAG_TISSUE=roots

YAG_SEQ=GTTCACGGG

BASE COUNT 175 a 127 c 157 g 193 t

ORIGIN

Query Match 18.3%; Score 356.2; DB 14; Length 652;

Best Local Similarity 71.8%; Pred. No. 7.1e-75;

Matches 466; Conservative 0; Mismatches 183; Indels 0; Gaps 0;

QY 937 GAGAGGGAGTTTCAGGAGAGGTTGAGATCATCATCAGAGATTCACCAAGCATCTGGT 996
 Db 1 GAACCTGAGTTTCAGGCGGAGTTGAGATCATCATCAGAGATTCACCAAGCATCTGGT 60
 QY 997 TCCTCTGTTGTTATTCATCGCGGTGCCAAGAAGTTGTTCTATGAGTTGTTCT 1056
 Db 61 TCCTCTGTTGTTATTCATCGCGGTGCCAAGAAGTTGTTCTATGAGTTGTTCT 120
 QY 1057 AACAAACATCTCGAGCTTCACCTCCATCGGCGGAGGAGGCGCTACAAAGTGAATGGAGCAC 1116
 Db 121 AATAACACCATGGAATCCACTTACATGGAAGATGCTCCGTAATGAGGATTCACCA 180
 QY 1117 AGATTGAAGATGCTCTGAGTCGCTAAGAGGATCTTCTATCTTCATGAGATGCAAT 1176
 Db 181 AGGCTGCGAATGCTCTGAGTGCCTAAGAGGATCTTCTATCTTCATGAGATGCAAT 240
 QY 1177 CCTAAATCATCTACCTGATATCAAGGCTTCAACATATATGATAGATTTCAAGTTCAA 1236
 Db 241 CCGAGATCATCTCGAGATATAAAGCTGCTAATATCTCTGATTTTCAATTTTGA 300
 QY 1237 GCTAAGTTGCTGATTTGCTTCTGCTTAAGATGCTTCTGATACAAACACGATGATCA 1296
 Db 301 GCAAGGTAGCGATTTGGCTTGGCAAGATTAATCTCCGATTTGCCACTCATGCTCG 360
 QY 1297 ACAGCTGATGGAACCTTTGGTACTTGGCTCCGGAATACGCTGCAAGCGGAAGCTC 1356
 Db 361 ACCGCTGATGGAAGTTTGGTACTTGGCTCCGGAATACGCTGCAAGCGGAAGCTC 420
 QY 1357 ACAGGAAGTCTGACGTTTCTCATTTGGCGTTGCTTTGGAGCTCATTAAGGAGCT 1416
 Db 421 TCAGATAATCTGATGTTTCTCATTTGCTTTGAGCTTTGAGATTAATCACTGGAAG 480
 QY 1417 CGACCGCTGATGCAACATGCTATGATGATGATGATGATGATGATGATGATGATGAT 1476
 Db 481 AGACCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 540
 QY 1477 TTGCTTAACGAGCATCTGAGGAGGAGACTTTGAGGTTTATGATGATGATGATGAT 1536
 Db 541 TTGCTTAACGAGCATCTGAGGAGGAGACTTTGAGGTTTATGATGATGATGATGAT 600
 QY 1537 AATGGGTATGACAGAGAGAGAGGCTTGGATGCTTGGTGTGCTGGG 1585
 Db 601 AAAGACTACACCATACGAGAGAGGCTTGGATGCTTGGTGTGCTGGG 649

RESULT 11
 BFI76907
 LOCUS
 DEFINITION EMI_4.B10.b1_A002 Embryo 1 (EM1) Sorghum bicolor cDNA, mRNA
 ACCESSION BFI76907
 VERSION BFI76907.1 GI:11064773
 KEYWORDS EST.
 SOURCE sorghum.
 ORGANISM Sorghum bicolor
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
 clade; Panicoideae; Andropogoneae; Sorghum.
 1 (bases 1 to 593)
 Reid,S.P., Cordonnier-Pratt,M.-M., Gingle,A. and Pratt,L.H.
 An EST database from Sorghum: developing embryos
 Unpublished (2000)
 Contact: Cordonnier-Pratt MM
 Laboratory for Genomics and Bioinformatics
 The University of Georgia, Department of Plant Biology
 Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
 Tel: 706 542 1850
 Fax: 706 583 0210
 Email: mmpratt@uga.edu
 Sequences have been trimmed to exclude PolyA, vector and regions
 below Phred quality 16. The threshold for highest quality sequence
 is 20.
 Seq primer: JEN REV

High quality sequence stop: 541
 POLYA=No.
 FEATURES
 source 1..593
 Location/Qualifiers
 /organism="Sorghum bicolor"
 /db_xref="taxon:4558"
 /clone_lib="Embryo 1 (EM1)"
 /note="Organ: Embryos germinated for 24 hr; Vector:
 pBluescript II from Lambda Zap II; Site 1: XhoI; Site 2:
 EcoRI; The library was made from poly-A RNA in the cloning
 vector lambda Zap II. Clones to be sequenced were
 prepared by mass excision."
 BASE COUNT 153 a 125 c 147 g 168 t
 ORIGIN

Query Match 18.0%; Score 349.2; DB 12; Length 593;
 Best Local Similarity 75.8%; Pred. No. 3.3e-73;
 Matches 432; Conservative 0; Mismatches 138; Indels 0; Gaps 0;
 QY 771 CTTCTCCAAAAGCATTTCACATACGAGGAGTCTAGAGCCACCAATGTTCTCGGA 830
 Db 17 CTCCTCGAAGACATTCACCTAGGAGAGTTGTTAGGGCACTGATGGTTCTCTGA 76
 QY 831 GCGAAGCTTTAGSACAAGGGGTTCTGTTACGTGCACAAAGTGTGTCCTAGTGG 890
 Db 77 TCTAATCTCTTGGCAAGGTTGTTGGGTATGTTTACAGAGGATGCTTCTTAATGG 136
 QY 891 GAAAGAAGTCTCTGGAAGCAGTTCAAAAGTTTGGAGTGTCTAGGAGAGGAGCTTCA 950
 Db 137 CAAAGAGATCTCTGTAAACAAATTTGAAAGTGTGCGAGGAGCGGTGATTCGA 196
 QY 951 GCGAGAGTTGAAATCATCAGCAGAGTTTCACACAGGATCTGTGTCTCTTTGGTTA 1010
 Db 197 GGCTGAGTTGAGATTATCAGCCGAGTACATCAACAACATCTGTGTCTTTGGTTA 256
 QY 1011 TTGATCCCGGTGCCAAAGATTTCTGTCTGTAGTTGTTCTCTACACAATCTCTGA 1070
 Db 257 TTGATTTCTGAGGAGGAGGTTGCTTGTCTGTAGTTGTTCTCTACACAATCTCTGA 316
 QY 1071 GCTTCACTCCATCGGAGGAGCGCTTACAAATGGAATGGAGCAGCAGATTAAGATTGC 1130
 Db 317 GTTCCACTTGTGATGGAAGATCGACCAACAATGGAGTGGCCACTAGATTAAAGATCG 376
 QY 1131 TCTTGGATCTGATAAGGACTTTCTTATCTTCTATGAAGATTGCAATCTCTAAATCAATCA 1190
 Db 377 TCTGGTGTGCGCAAGGTTTAGCTTATCTTCTATGAAGACTGCCATCCGAAGATCATCA 436
 QY 1191 CCGTGATATCAAGCTTCAACATATTCATAGATTTCAGTTTGAAGTTCAGCTAGGTTGCTGA 1250
 Db 437 CCGTGATATCAAGGCTTCAACATATTCATAGATTTCAGTTTGAAGTTCAGCTAGGTTGCTGA 496
 QY 1251 TTTTGGTCTTGAAGATTGCTTCTGATACAAACACCGCATGTATATCAACACGCTGATGGG 1310
 Db 497 TTTTGGACTTGAAGTTCACTACTGATAACAACACTCATCTTTCGACAGAGTAATGGG 556
 QY 1311 AACCTTGGGTACTTGGCTCGGAATAGCG 1340
 Db 557 CACCTTTGGGTATTTTGGCGCTGATGTC 586

RESULT 12
 BQ240617
 LOCUS
 DEFINITION TAE05015B02R TAE05 Triticum aestivum cDNA clone TaE05015B02R, mRNA
 ACCESSION BQ240617
 VERSION BQ240617.1 GI:20436493
 KEYWORDS EST.
 SOURCE bread wheat.
 ORGANISM Triticum aestivum
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae
 ; Triticeae; Triticum.

1. (bases 1 to 646)
 Cloutier, S.
 Wheat functional genomics - Glerlea developing seeds cDNA libraries
 Unpublished (2002)
 Contact: Dr. Sylvie Cloutier
 Cereal Research Centre, Agriculture and Agri-food Canada
 195 Dafoe Rd, Winnipeg, MB, Canada R3T 2M9
 Tel: (204) 983-2340
 Fax: (204) 983-4604
 Email: scloutier@em.agr.ca
 was cloned directionally, not all sequences generated with reverse
 primer were from the 5' end (same with forward primer and 3' end).
 Average insert size is >2.0 kb
 Plate: 015 row: B column: 02
 Seq primer: M13 Reverse.

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FEATURES             source
Location/Qualifiers
1. .646
   /organism="Triticum aestivum"
   /cultivar="Glenlea"
   /db_xref="taxon:4565"
   /clone="raE05015B02R"
   /clone_lib="raE05"
   /tissue_type="developing seeds"
   /dev_stage="5 days after anthesis"
   /lab_host="E. coli DH10B"
   /note="Vector: pSPORT-P (Invitrogen Technologies); Site-1:
NotI; Site-2: MluI; mRNA obtained from wheat seeds of
cultivar Glenlea 5 days post-anthesis"
163 a 126 c 162 g 189 t
BASE COUNT
ORIGIN

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Query Match 17.9%; Score 348.6; DB 14; Length 646;
Best Local Similarity 71.8%;
Pred. No. 4.3e-73;
Matches 456; Conservative 0; Mismatches 179; Indels 0; Gaps 0;

| | | | | | | | |
|------|----|---------------|---------------|---------------|-------------------|---------------------------------|------|
| 957 | QY | GGTGTGATCATCA | CAGCAGAGTTCC | ACCACAGGCATCT | GGTGTCTCTTCTG | TCTGTTATTCGCAT | 1016 |
| | | | | | | | |
| 12 | Db | SGTTGAGATTAC | AGCGCGCTTCAT | CACAGCATCTGTG | TCTGTTGGTTACTGCAT | 71 | |
| | | | | | | | |
| 1017 | QY | CGCGGTGCCAA | AGAATGCTTGTCT | TAAGTTTGTTCCT | TAACAACAATCTC | GAGTTCA 1076 | |
| | | | | | | | |
| 72 | Db | CTCTGGGGGA | AGAGTTGCTTAT | ATAGTTTGTCA | CCAAATAACACAT | TGGATTTCCA 131 | |
| | | | | | | | |
| 1077 | QY | CTTCCATGGG | AGGAGCGGCT | ACATGGAATG | SGAGCACCAGAT | TGAAGATTGCTTTGG 1136 | |
| | | | | | | | |
| 132 | Db | CTTACATGGA | AAAGGCGTCC | AAAGTTGGGAGT | CGCCATAAAGACT | TAGGATTGCCCTTGG 1191 | |
| | | | | | | | |
| 1137 | QY | ATCTGCTAA | AGGACTTTCTTA | CTTCATGAAGAT | TGCAATCCTTA | AAATCATATCACGTTGA 1196 | |
| | | | | | | | |
| 192 | Db | TGCTGCTA | AGGTTTGGCAT | TCATTCATG | AGATTGCCACCG | AGATCAATCATCGTGA 251 | |
| | | | | | | | |
| 1197 | QY | TATCAAGGCT | TCAACATATT | GTATGATTTCA | AGTTTGAAGCTTA | AGGTTGCTGATTTTGG 1256 | |
| | | | | | | | |
| 252 | Db | TATAAAGTC | ATCAAAACAT | TCTTCTGATT | TAAATCAAGCT | TAAAGTTGCGGATTTGG 311 | |
| | | | | | | | |
| 1257 | QY | TCTTGCTAA | GATTGCTTCT | GTATCAAA | ACGCGATGATCA | ACAGTGTGATGGGAACCTT 1316 | |
| | | | | | | | |
| 312 | Db | CTGGCAAA | AGTTTCCCTCT | GTATGA | AAACACACATG | TGTCAACAAGAGTAATATGGGCACATT 371 | |
| | | | | | | | |
| 1317 | QY | TGGGTACTT | GGGTCGCG | GAATAGCTG | CNAGCGGAAGCT | CTACGAGAAAGTCTGACGTTT 1376 | |
| | | | | | | | |
| 372 | Db | TGGGTATCT | AGCACCAG | AATGCGTCT | TCTGGAAAGCT | TAACCTGAGAAATCAGATGCTTT 431 | |
| | | | | | | | |
| 1377 | QY | CTCATTTGG | CGTTTGCTTTT | GGAGCTCAT | TACTTGGACGCT | TCGACCGGTTTGA TGCCACAA 1436 | |
| | | | | | | | |
| 432 | Db | TTCCTTTGG | AGTGAIGCTT | CTTGGAGCT | GTATACTGGGCGT | GTGATTCGACCCA 491 | |
| | | | | | | | |
| 1437 | QY | TGCTATGTA | GTAGACAGCT | TAGTTGACT | SGGACGACCAT | TGCTTAACCGAGCACTGA 1496 | |
| | | | | | | | |
| 492 | Db | AAACATAT | ATGGATGACAG | CTTGTTGATT | GGCAAGACCTT | TACTGATCGGAGCACTGA 551 | |
| | | | | | | | |
| 1497 | QY | GCAAGGAG | ACTTGTAGG | GGTTTACGTG | ATCGCAAAAGT | TGAATATGGGTATGACAGAGGA 1556 | |
| | | | | | | | |

| | | | | | |
|------------|---------------|--|-------------|----------------------------------|-----------------|
| 552 | GGATGGTA | CTATGATG | AGTTAGT | GGATGCTGCTGGGAAGGATTTCAATCTAATGA | 611 |
| | | | | | |
| 1557 | GATGGCTCGCATG | GTTCCTTGTG | GCTCGGCTTG | 1591 | |
| | | | | | |
| 612 | GATGGCCAGATG | ATAGCATGTGCTGCTGCATGTG | 646 | | |
| | | | | | |
| RESULT | 13 | | | | |
| BQ134241 | | | | | |
| LOCUS | | BQ134241 | 637 bp | linear | EST 19-APR-2002 |
| DEFINITION | | 1991014D01.Y2 1091 - Immature ear with common ESTs screened by | | | |
| | | Schmidt lab Zea mays cDNA, mRNA sequence. | | | |
| ACCESSION | | BQ134241 | | | |
| VERSION | | BQ134241.1 | GI:20208152 | | |

| KEYWORDS | EST. | |
|-----------|--|--|
| SOURCE | SOURCE | |
| ORGANISM | ORGANISM | |
| | Zea mays. | |
| | Zea mays | |
| | Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Zea. | |
| REFERENCE | 1 (bases 1 to 637) | |
| AUTHORS | Walbot,V. | |
| TITLE | Maize ESTs from various cDNA libraries sequenced at Stanford University | |
| JOURNAL | Unpublished (1999) | |
| COMMENT | Contact: Walbot V | |
| | Department of Biological Sciences | |
| | Stanford University | |
| | 855 California Ave, Palo Alto, CA 94304, USA | |
| | Tel: 650 723 2227 | |
| | Fax: 650 723 8221 | |
| | Email: walbot@stanford.edu | |
| | Plate: 1091014 row: D column: 01. | |

```

FEATURES
source
location/Qualifiers
1. .637
/organism="Zea mays"
/cultivar="OH43"
/db_xref="taxon:4577"
/clone_lib="1091 - Immature ear with common ESTs screened
by schmidt lab"
/tissue_type="Inflorescence meristem - floral organ
primordia"
/dev_stage="0.5 cm to 2 cm"
/lab_host="Stratagene XLOIR"
/note="Organ: immature ear; Vector: pMD-GAL4; Site_1:
EcoRI; Site_2: XhoI; RNA from library 606 was filtered for
common ESTs found in 606."
165 a 133 c 156 g 183 t
BASE COUNT

```

| Query Match | 17.9% | Score 348.2 | DB 14 | Length 637 |
|-----------------------|----------------|----------------------------|--|------------|
| Best Local Similarity | 73.2% | Pred. No. 5.9e-73 | | |
| Matches 446 | Conservative 0 | Mismatches 163 | Indels 0 | Gaps 0 |
| QY | 712 | GGCTCCGACTACTCGGACCG | GCAGTCTTCTCTCCACCGTCTCCAGGGCTGTGTAGGC | 771 |
| Db | 29 | GGTCTAAATTACTCTGTGGCGAGAT | CTCTACCTCCACCATCCCTGGTCTGTCTTGGC | 88 |
| QY | 772 | TTCTCCAAAAGCACTTTCACATAC | ACGAGGAGCTAGCTAGAGCCACCAATGGTTTCCCGAG | 831 |
| Db | 89 | TTCTCGAAGGCACATTTCTACCTAC | GANGAGGCTGTGAGGGCTACTGATGGATTTCCGAT | 148 |
| QY | 832 | CGCAACTCTGTATGAGCAAGCGGG | TTTCGGTTACGTCGCAAAAGGTGTCTTGCCTAGTGGG | 891 |
| Db | 149 | GCATATCTCTTGGACAAGGTG | TTTGTATTATGTTTACATATGATTTCTGCCCTAATGGC | 208 |
| QY | 892 | AAAGAAGTTCGTGTGAAGCAGTTG | AAAGTTGGAGTGTCTCAGGAGAGAGGAGGTTTCAG | 951 |
| Db | 209 | AAAGAGATTTCGTGTAATAACAATT | GAACTGGGAAGTGGCCAGGGAGACGCTGAGTTCAG | 268 |
| QY | 952 | GCAGAGGTTGAGATCATCAGCAGAG | TTCACCAACAGGCATCTGGTGCTCTCTTGTGGTTAT | 1011 |
| Db | 269 | GCTGAGGTTGAGATTATCAGCCAGAT | CATCATCAAAACACCTTGTCTTTGGTGGGTTAT | 328 |

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 2, 2003, 15:16:17 ; Search time 25 Seconds
(without alignments)
1073.407 Million cell updates/sec

Title: US-10-086-464-2

Perfect score: 3453

Sequence: 1 MSSAPSPGTGPPSPSPNST.....REMEMGKIKRTGGYSGPSL 647

Scoring table: BZOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match % | Length | ID | Description |
|------------|-------|---------------|--------|--------------|---------------------|
| 1 | 656.5 | 19.0 | 410 | 1 APKA_ARATH | Q06548 arabidopsis |
| 2 | 654.5 | 19.0 | 412 | 1 APKB_ARATH | P46573 arabidopsis |
| 3 | 647.5 | 18.8 | 942 | 1 TMK1_ARATH | P43298 arabidopsis |
| 4 | 636.5 | 18.1 | 389 | 1 NAK_ARATH | P43293 arabidopsis |
| 5 | 605 | 17.5 | 901 | 1 CLV1_MAIZE | Q24585 zea mays (m |
| 6 | 579.5 | 16.8 | 390 | 1 CR14_ARATH | Q85Y98 arabidopsis |
| 7 | 572 | 16.5 | 849 | 1 SRK6_BRAOL | Q09092 brassica ol |
| 8 | 525 | 15.2 | 399 | 1 RLK5_ARATH | P47735 arabidopsis |
| 9 | 515.5 | 14.9 | 716 | 1 TRAL_MOUSE | Q62406 mus musculu |
| 10 | 512.5 | 14.8 | 817 | 1 KPRO_MAIZE | P17801 zea mays (m |
| 11 | 500 | 14.5 | 712 | 1 TRAL_HUMAN | P51617 homo sapien |
| 12 | 434 | 12.6 | 555 | 1 GPL_CHLRE | Q9FDQ6 chilanydomon |
| 13 | 374 | 10.8 | 674 | 1 TML1_ARATH | P33543 arabidopsis |
| 14 | 367.5 | 10.6 | 501 | 1 KPEL_DROME | Q05652 drosophila |
| 15 | 360 | 10.4 | 620 | 1 EXTN_TOBAC | P13983 nicotiana t |
| 16 | 355 | 10.3 | 296 | 1 PRP3_MOUSE | P05143 mus musculu |
| 17 | 353 | 10.2 | 1490 | 1 CRK7_HUMAN | Q9HYV4 homo sapien |
| 18 | 348 | 10.1 | 913 | 1 DDRL_HUMAN | Q08345 h epithelia |
| 19 | 346.5 | 10.0 | 267 | 1 EXTN_MAIZE | P14918 zea mays (m |
| 20 | 342 | 9.9 | 5179 | 1 MOC2_HUMAN | Q02817 homo sapien |
| 21 | 337 | 9.8 | 261 | 1 PRP2_MOUSE | P05142 mus musculu |
| 22 | 332 | 9.6 | 426 | 1 EXLP_TOBAC | Q03211 nicotiana t |
| 23 | 329.5 | 9.5 | 807 | 1 RMIL_COTJA | P34908 coturnix co |
| 24 | 329.5 | 9.5 | 1584 | 1 KYK1_DICDI | P18160 dictyosteli |
| 25 | 328.5 | 9.5 | 743 | 1 EXT2_ARATH | Q9mlg9 arabidopsis |
| 26 | 326.5 | 9.5 | 911 | 1 DDRL_MOUSE | Q03146 mus musculu |
| 27 | 325 | 9.4 | 806 | 1 RMIL_CHICK | Q04982 gallus gall |
| 28 | 324.5 | 9.4 | 910 | 1 DDRL_RAT | Q63474 rattus norv |
| 29 | 323.5 | 9.4 | 283 | 1 EXTN_SORBI | P24152 sorghum bic |
| 30 | 320 | 9.3 | 1174 | 1 KPCL_COCHC | O42632 cochllobol |
| 31 | 319 | 9.2 | 590 | 1 TRAZ_HUMAN | O43187 homo sapien |
| 32 | 318.5 | 9.2 | 1386 | 1 ZAP3_MOUSE | Q39017 mus musculu |
| 33 | 316 | 9.2 | 503 | 1 WAIP_HUMAN | O43516 homo sapien |

ALIGNMENTS

RESULT 1

| ID | APKA_ARATH | STANDARD; | PRT; | 410 AA. |
|----|---|-----------|------|---------|
| AC | Q06548; | | | |
| DT | 01-NOV-1995 (Rel. 32, Created) | | | |
| DT | 01-NOV-1995 (Rel. 32, Last sequence update) | | | |
| DT | 16-OCT-2001 (Rel. 40, Last annotation update) | | | |
| DE | Protein kinase APK1A (EC 2.7.1.-). | | | |
| GN | APK1A. | | | |
| OS | Arabidopsis thaliana (Mouse-ear cress). | | | |
| OC | Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; | | | |
| OC | Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; | | | |
| OC | eurosid II; Brassicales; Brassicaceae; Arabidopsi. | | | |
| OX | NCBI_TaxID=3702; | | | |
| RN | [1] | | | |
| RP | SEQUENCE FROM N.A. | | | |
| RC | STRAIN=cv. Columbia; | | | |
| RX | MEDLINE=93081726; PubMed=1450380; | | | |
| RA | Hirayama T., Oka A.; | | | |
| RT | "Novel protein kinase of Arabidopsis thaliana (APK1) that phosphorylates tyrosine, serine and threonine."; | | | |
| RL | Plant Mol Biol. 20:653-662(1992) | | | |
| CC | !- FUNCTION: POSSIBLE BI-FUNCTIONAL KINASE. IN VITRO, IT EXHIBITS SERINE/THREONINE ACTIVITY. IN VIVO, CAN PHOSPHORYLATE TYROSINE RESIDUES OF LIMITED SUBSTRATES. | | | |
| CC | !- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES. | | | |
| CC | This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch). | | | |
| CC | EMBL; D12522; BAA02092.1; - | | | |
| DR | InterPro; IPR000719; Euk_pkinase. | | | |
| DR | InterPro; IPR0004040; STY_pkinase. | | | |
| DR | InterPro; IPR002290; Ser_thr_pkinase. | | | |
| DR | Pfam; PF00069; pkinase; 1. | | | |
| DR | ProDom; PD000001; Euk_pkinase; 1. | | | |
| DR | SMART; SM00221; STYK; 1. | | | |
| DR | PROSITE; PS00107; PROTEIN_KINASE_ATP; 1. | | | |
| DR | PROSITE; PS00108; PROTEIN_KINASE_ST; 1. | | | |
| DR | PROSITE; PS50011; PROTEIN_KINASE_DOM; 1. | | | |
| KW | Transferase; Serine/threonine-protein kinase; Tyrosine-protein kinase; | | | |
| KW | ATP-binding; Multigene family; Myristate. | | | |
| FT | LIPID 2 2 MIRISTATE (BY SIMILARITY). | | | |
| FT | DOMAIN 68 352 PROTEIN KINASE. | | | |
| FT | NP_BIND 74 82 ATP (BY SIMILARITY). | | | |
| FT | BINDING 106 106 ATP (BY SIMILARITY). | | | |
| FT | ACT_SITE 203 203 BY SIMILARITY. | | | |
| SQ | SEQUENCE 410 AA; 45519 MW; 5BAR28D9E0065082 CRC64; | | | |

Query Match 19.0%; Score 536.5; DB 1; Length 410;
Best Local Similarity 39.1%; Pred. No. 1.4e-18;

Q05609 arabidopsis
P04280 homo sapien
P07527 schizosacch
O9J104 mus musculu
O60610 homo sapien
P06599 daucus caro
P46551 caenorhabdi
P28693 gallus galli
O08308 mus musculu
P43562 saccharomyc
P23246 homo sapien
P37370 saccharomyc

34 315 9.1 821 1 CRL_ARATH
35 312.5 9.1 331 1 P8P1_HUMAN
36 311 9.0 877 1 WEL_SCHPO
37 310.5 9.0 1567 1 FMN2_MOUSE
38 307 8.9 1248 1 DIAL_HUMAN
39 306.5 8.9 306 1 EXTN_DAUCA
40 300.5 8.7 684 1 CDK9_CAEEL
41 300.5 8.7 1004 1 EPB2_CHICK
42 297.5 8.6 1255 1 DIAL_MOUSE
43 297 8.6 842 1 CLA4_YEAST
44 296.5 8.6 707 1 SFPQ_HUMAN
45 296.5 8.6 817 1 VRP1_YEAST

Matches 160; Conservative 63; Mismatches 131; Indels 55; Gaps 12;

QY 238 GSDYDRPVLPPP-----SPGLVLFESKSTIYEELARATNGFSEANLGGGFGYV 289
 DB 29 GSKASSVYRPSFPRTEGEILOSPNL-----KSFSAELKSAFNRPRDSVLGGGFGCV 82
 QY 290 HGVLP-----SGKEVAVKLVGGGQGERFOAEVETISRVHRHLVSLVGYCI 339
 DB 63 FKGWIDEKSLTASRPTGLVIAVKKLNDQWGHQEWLAENVYLGQFSRHLVKLGYCL 142
 QY 340 AGAKRLVYEEFVNNLEHLHGG--RPTWENSTRKIALGSAKGLSYLHEDCNPKII 396
 DB 143 EDEHLVYEEFVNNLEHLHGG--RPTWENSTRKIALGSAKGLSYLHEDCNPKII 396
 QY 397 HRDIKASNLIDFKFEAKVADFLAKIAS-DNTHTVSTRVMGTGFLAPEYLAASGLTK 455
 DB 201 YRDFKTSNILLDSYNAKLSDFGLAKDGPIGOKSHVSTVMTGTHYAAPEYLAIGHLT 460
 QY 456 SDVYFSGVYVLLITGRPPVDANNVYVDSLVDMARPLNRASEQDFEGLADAKNNGY 515
 DB 261 SDVYFSGVYVLLITGRPPVDANNVYVDSLVDMARPLNRASEQDFEGLADAKNNGY 515
 QY 516 DREEMARVACAAACVRSARRPRMSQIVRALEGVSLSDINEGHRPQSNVSYSGS 575
 DB 318 SWEZACKVATLSRLCTTEIKLRPNKSEVVSLEHIOISLN-----AAIGN 363
 QY 576 TDYDSQY--NEDMKFRKMAIGTQETNATGEYSNPTSDYGLYPSGSS 622
 DB 364 MDKTDRRMRSSDSVSVKKNAGFAQTAVG-----STVVAYPRPSAS 406

RESULT 2

APKB_ARATH STANDARD; PRT; 412 AA.

ID APKB_ARATH STANDARD; PRT; 412 AA.

AC P46573; Q9SLH5; (Rel. 32, Created)

DT 01-NOV-1995 (Rel. 40, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DE Protein kinase APKIB (EC 2.7.3.-)

GN APKIB OR AT2G28930 OR T914.1.

OS Arabidopsis thaliana (Mouse-ear cross).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;

OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.

OX NCBI_taxid=3702;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=cv. Columbia;

RX MEDLINE=20083487; PubMed=10617137;

RA Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,

RA Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblum T.V.,

RA Buehl K.S., Ketchum K.A., Lee J.J., Ronning C.M., Koo H.L.,

RA Moffat K.S., Cronin L.A., Shen M., Pai G., Van Aken S., Umayam L.,

RA Tallon L.J., Gill J.E., Adams M.D., Carrera A.J., Creasy T.H.,

RA Goodman H.M., Somerville C.R., Copenhaver G.P., Preuss D.,

RA Niernan W.C., White O., Eisen J.A., Salzberg S.L., Fraser C.M.,

RA Venter J.C.;

RT "Sequence and analysis of chromosome 2 of the plant Arabidopsis

RT thaliana.";

RL Nature 402:761-768(1999).

RN [2]

RP SEQUENCE OF 143-346 FROM N.A.

RC STRAIN=cv. Columbia;

RX MEDLINE=93081726; PubMed=1450380;

RA Hirayama T., Oka A.;

RT "Novel protein kinase of Arabidopsis thaliana (APK1) that

RT phosphorylates tyrosine, serine and threonine.";

RL Plant Mo. Biol. 20:653-662(1992).

CC -!- FUNCTION: POSSIBLE BI-FUNCTIONAL KINASE. IN VITRO, IT EXHIBITS

CC SERINE/THREONINE ACTIVITY. IN VIVO, CAN PHOSPHORYLATE TYROSINE

CC RESIDUES OF LIMITED SUBSTRATES (BY SIMILARITY).

CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.

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CC or send an email to license@isb-sib.ch).

EMBL; AC005315; AAC33221.1; --

EMBL; D10152; BAA20968.1; --

InterPro; IPR000719; Euk_pkinase.

InterPro; IPR004040; STY_pkinase.

InterPro; IPR002290; Ser_thr_pkinase.

InterPro; IPR001245; Tyr_pkinase.

Pfam; PF00089; pkinase; 1.

PRINTS; PR00109; TYRKINASE.

ProDom; PD000001; Euk_pkinase; 1.

SMART; SM00221; STYK; 1.

PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.

PROSITE; PS00108; PROTEIN_KINASE_ST; 1.

PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.

KW Transferase; Serine/threonine-protein kinase; Tyrosine-protein kinase;

KW ATP-binding; Multigene family; Myristate.

FT LIPID 2 2 MYRISTATE (BY SIMILARITY).

FT DOMAIN 69 356 PROTEIN KINASE.

FT NP_BIND 75 83 ATP (BY SIMILARITY).

FT BINDING 107 107 ATP (BY SIMILARITY).

FT ACT_SITE 204 204 BY SIMILARITY.

FT ACT_SITE 204 204 BY SIMILARITY.

SQ SEQUENCE 412 AA; 45746 MW; EB1CA0B1A626A5DA CRC64;

Query Match 19.0%; Score 654.5; DR 1; Length 412;

Best Local Similarity 41.3%; Pred. No. 1.7e-18;

Matches 152; Conservative 62; Mismatches 113; Indels 41; Gaps 11;

QY 226 PPPPPFMS-----SGGSDYSRPLVPPP-----SPGLVLFESKSTIYEELARATN 273
 DB 14 PGASPKYMSSEANDSLGSKSSVSININPTREGEILOSPNL-----KSFSAELAAAF 67
 QY 274 GFSEANLGGGFGYVHKGVLP-----SGKEVAVKLVGGGQGERFOAEVETI 323
 DB 68 NFRPDSVLGGGFGYVHKGVLP-----SGKEVAVKLVGGGQGERFOAEVETI 323
 QY 324 SRVHRHLVSLVGYCIAGAKRLVYEEFVNNLEHLHGG--RPTWENSTRKIALGSA 381
 DB 128 GQFHPNLVKLIGYCLEDEHRLVYEEFVNNLEHLHGG--RPTWENSTRKIALGSA 381
 QY 382 KGLSYLHEDCNPKIIHRDIKASNLIDFKFEAKVADFLAKIAS-DNTHTVSTRVMGTG 440
 DB 188 KGLAFLH-NAETSVIYRDFKTSNILLDSYNAKLSDFGLAKDGPIGOKSHVSTVMTG 246
 QY 441 YLAPEYLAASGLTKESDVFSGVYVLLITGRPPVDANNVYVDSLVDMARPLNRASEQ 500
 DB 247 YAAPEYLAAGHLTKSDVYSYGVVLLITGRPPVDANNVYVDSLVDMARPLNRASEQ 500
 QY 501 GDFEGLADAKNNGYDREEMARVACAAACVRSARRPRMSQIVRALEGVSLSDINEG 560
 DB 305 KLFER-VIDNRLQDQYSMEACKVATLALRCITFEIKLRPNKSEVVSLEHIOISLN 360
 QY 561 MRPGQSNV 568
 DB 361 ---GGRN 365

RESULT 3

TMK1_ARATH STANDARD; PRT; 942 AA.

ID TMK1_ARATH STANDARD; PRT; 942 AA.

AC P43293;

DT 01-NOV-1995 (Rel. 32, Created)

DT 01-NOV-1995 (Rel. 32, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE Putative receptor protein kinase TMK1 precursor (EC 2.7.1.-).

CC TMK1 OR AT1G56150 OR F15E12.4.

OS Arabidopsis thaliana (Mouse-ear cross).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
 OX NCBL_TaxID=3702;
 RN [-;
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv, Columbia;
 RX MEDLINE=93076110; PubMed=1332795;
 RA Chang C., Schaller G.E., Patterson S.E., Kwok S.F.,
 RA Meyerowitz E.M., Bleecker A.B.;
 .RT "The TMK1 gene from Arabidopsis codes for a protein with structural
 .RT and biochemical characteristics of a receptor protein kinase.";
 RL Plant Cell 4:1263-1271(1992).
 RN [2;
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv, Columbia;
 RX MEDLINE=21016719; PubMed=11130712;
 RA Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,
 RA White O., Alonso J., Altati H., Araujo R., Bowman C.L., Brooks S.Y.,
 RA Buehler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,
 RA Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,
 RA Dunn P., Etgu P., Feldblum T.V., Feng J.-D., Fong B., Fujii C.Y.,
 RA Gill J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Huizar L.,
 RA Hurter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,
 RA Kim C.J., Koo H.L., Kremenetskaia I., Kurtz D.B., Kwan A., Lam B.,
 RA Langin-Hooper S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li X.-P.,
 RA Lin X., Liu S.X., Liu Z.A., Lueros J.S., Maiti R., Marziani A.,
 RA Militscher J., Miranda M., Nguyen M., Nierman W.C., Osborne B.I.,
 RA Pai G., Peterson J., Pham P.K., Rizzo M., Rooney T., Rowley D.,
 RA Sakano H., Salzberg S.L., Schwartz J.R., Shinn P., Southwick A.M.,
 RA Sur H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D.,
 RA Uterback T., Van Aken S., Vaysberg M., Vysotskaia V.S., Walker M.,
 RA Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.;
 .RT "Sequence and analysis of chromosome 1 of the plant Arabidopsis
 .RT thaliana.";
 RL Nature 408:816-820(2000).
 CC [-; FUNCTION: PROBABLE RECEPTOR.
 CC [-; SUBCELLULAR LOCATION: Type I membrane protein.
 CC [-; TISSUE SPECIFICITY: FOUND IN MOST TISSUES.
 CC [-; PTM: AUTOPHOSPHORYLATED ON SERINE AND THREONINE RESIDUES.
 CC [-; SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 CC [-; SIMILARITY: CONTAINS 9 LEUCINE-RICH REPEATS (LRR).
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: L00670; AAA32876.1; -;
 CC DR EMBL; AC026480; AAG51302.1; -;
 CC DR HSSP: P12931; 1PMK.
 CC DR InterPro: IPR000719; Euk_pkinase.
 CC DR InterPro: IPR001611; LRR.
 CC DR InterPro: IPR003592; LRR_out.
 CC DR InterPro: IPR003591; LRR_tyr.
 CC DR InterPro: IPR004040; STY_pkinase.
 CC DR InterPro: IPR002290; Ser_thr_pkinase.
 CC DR Pfam: PF00069; pkinase; 1.
 CC DR Pfam: PF03560; LRR; 11.
 CC DR ProDom: PD000001; Euk_pkinase; 1.
 CC DR SMART: SM00370; LRR; 7.
 CC DR SMART: SM00369; LRR_TYR; 1.
 CC DR SMART: SM00221; STYK; 1.
 CC DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
 CC DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
 CC DR PROSITE: PS00011; PROTEIN_KINASE_DOM; 1.
 CC DR Transferase: Serine/threonine-protein kinase; ATP-binding;
 CC Transmembrane; Receptor; Glycoprotein; Signal; Repeat;
 CC Leucine-rich repeat; Phosphorylation.
 CC SIGNAL 1 23
 CC POTENTIAL.

| | | | |
|-------------|---------|------------|--|
| FT CHAIN | 24 | 942 | PUTATIVE RECEPTOR PROTEIN KINASE TMK1. |
| FT DOMAIN | 24 | 482 | EXTRACELLULAR (POTENTIAL). |
| FT TRANSMEM | 483 | 503 | POTENTIAL. |
| FT DOMAIN | 504 | 942 | CYTOPLASMIC (POTENTIAL). |
| FT REPEAT | 87 | 110 | LRR 1. |
| FT REPEAT | 111 | 133 | LRR 2. |
| FT REPEAT | 135 | 159 | LRR 3. |
| FT REPEAT | 185 | 209 | LRR 4. |
| FT REPEAT | 231 | 253 | LRR 5. |
| FT REPEAT | 254 | 278 | LRR 6. |
| FT REPEAT | 280 | 300 | LRR 7. |
| FT REPEAT | 385 | 408 | LRR 8. |
| FT REPEAT | 409 | 436 | LRR 9. |
| FT DOMAIN | 589 | 869 | PROTEIN KINASE. |
| FT NP_BIND | 594 | 602 | ATP (BY SIMILARITY). |
| FT BINDING | 616 | 616 | ATP (BY SIMILARITY). |
| FT ACT_SITE | 717 | 717 | BY SIMILARITY. |
| FT CARBOHYD | 86 | 86 | N-LINKED (GLCNAC. .) (POTENTIAL). |
| FT CARBOHYD | 99 | 99 | N-LINKED (GLCNAC. .) (POTENTIAL). |
| FT CARBOHYD | 158 | 158 | N-LINKED (GLCNAC. .) (POTENTIAL). |
| FT CARBOHYD | 164 | 164 | N-LINKED (GLCNAC. .) (POTENTIAL). |
| FT CARBOHYD | 171 | 171 | N-LINKED (GLCNAC. .) (POTENTIAL). |
| FT CARBOHYD | 230 | 230 | N-LINKED (GLCNAC. .) (POTENTIAL). |
| FT CARBOHYD | 285 | 285 | N-LINKED (GLCNAC. .) (POTENTIAL). |
| FT CARBOHYD | 363 | 363 | N-LINKED (GLCNAC. .) (POTENTIAL). |
| FT CARBOHYD | 397 | 397 | N-LINKED (GLCNAC. .) (POTENTIAL). |
| SQ SEQUENCE | 942 AA; | 102387 MW; | 93E300B52FF549DE CRC64; |

Query Match 18.8%; Score 647.5; DB 1; Length 942;
 Best Local Similarity 30.8%; Pred. No. 6.1e-18;
 Matches 178; Conservative 90; Mismatches 194; Indels 115; Gaps 17;

| | | | |
|--------|---|---|----------------|
| QY 104 | VPGPSNP | -----SREGGSPRPSPSPSPSPSDGLS----- | -----TGVVV 140 |
| DB 426 | VPGRSVNVVINGNPDIGKDKSLSSPGSSSGSGSGINGDKDRCKMSSTFGIIV | 485 | --- |
| QY 141 | GTAIGGVALLVTVTLICLLCKKRR | -----DEEDAYVYPPPPGPRAGGPGGQQQW 195 | --- |
| DB 486 | GSVLGGLSIFLIGLLVFCWYKKRKRFSGSSNAVVHP | ----- | 526 |
| QY 196 | RQQAATPPSDHVVTSLPAPPKAPSPPPPPPPPPPPSSSGGSDYSDRPVLPSPS | ----- | 251 |
| DB 527 | RHSGSDNESVKTVA | -----GSSVSVGGSIDTYITLPGTSEVCE 564 | --- |
| QY 252 | -----PGLVLGFSKSTFTYEELARATNGFSANLLGGGFGYVHKVLPSSKRYAVKQL 305 | --- | --- |
| DB 565 | NIQMYEAGNML | -----ISIQVLRSVTNNFSSDNILGSGFGWYKGLHDGKTIAVKRM 618 | --- |
| QY 306 | KVG--SGGGEREFOAEVILISVHRHLVSLVGYCIAGAKRLLVYEFVNNHLEHL | ----- | 360 |
| DB 619 | ENGYIAGKGFAEKSEIAVLKVRHRLVLLGYCLDNEKLVLYEYMPGGTLSRHLFEW 678 | --- | --- |
| QY 361 | HGEGRPTMESTRLKIALGSAKGLSYLHEDCNPKIHRDIKASNLIDFKPEAKVADFGL 420 | --- | --- |
| DB 679 | SEGLKPLLWKQRLTALDVARVYELHGLAQHSFIHDLKPSNILLGDMRAKVADEGL 738 | --- | --- |
| QY 421 | AKIASDTHVHSTRVMGTFGLAPEYAAASKLTKESDVFSFGVLELITGRPPVDANNV 480 | --- | --- |
| DB 739 | VRLAPEGKGSITRIAGTFGLAPEYAVTGRVTVKVDYVSFGVILMELITGRKSLDESQP 798 | --- | --- |
| QY 481 | YVEDSLVDWARPLLNRASEOGDEGLADAKNNGVDREMA | -----RMVACAAACVRSARR 537 | --- |
| DB 799 | EESTHLVSWFARMY--INKEASFKAIDTTID--LDEETLASVHTVVAELAGHCACAREPYQ 854 | --- | --- |
| QY 538 | RPRMSQIVRALEGVNSLDLNEGMRPGOSNVYSYGGSTDYDSSQYNDNEMKKFKMALGT 597 | --- | --- |
| DB 855 | RPDMGHAV-----NL-LSSLVELMKPSONEDYIG--IDLDMSLPQALKKQAYEGRS 905 | --- | --- |
| QY 598 | QEYNATG-----EFSNFTSDYGLYPSGSSSEGG 625 | --- | --- |
| DB 906 | DLESSTSLPLSLONTQMSITRPGFAESFTSDVGR 942 | --- | --- |

DR SMART; SM00221; STYK; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
KW Transferrase; Serine/threonine-protein kinase; ATP-binding.
FT DOMAIN 68 353 PROTEIN KINASE.
FT NP_BIND 74 82 ATP (BY SIMILARITY).
FT BINDING 106 106 ATP (BY SIMILARITY).
FT ACT_SITE 203 203 BY SIMILARITY.
FT CONFLICT 287 287 G -> V (IN REF. 1).
SQ SEQUENCE 389 AA; 43533 MW; 58A11A78515898E3 CRC64;
Query Match 18.1%; Score 626.5; DB 1; Length 389;
Best Local Similarity 41.1%; Pred No. 1.7e-113; Indels 19; Gaps 7;
Matches 137; Conservative 64; Mismatches 113;
QY 232 FMSSSG--GSDYSDRPVLPSPSPGLVGLGFSKSTFTYELARATNGFSEANLIGSGFGYV 289
Db 23 FLSDKSGKSTASFSYMPRTGEHILQANLNFSLSELKASATRNRPDSVVVGGFGCV 82
QY 290 HKG-----VLPS---GKGVAKVLKVGSGGREFQAEVILSRVHRLHSLVGYCI 339
Db 83 FKGVDESSLAPSKPGTGIVAVKRLNQEGFGQHREWLAEINYLQGLDHPNLVKLIGYCL 142
QY 340 AGAKRLVYEFVNNNLHLHGEGR--PTMWSLTKIALGSAKGLSYLHEDCNPKIHH 397
Db 143 EEEHRLVYEFMTRGSLNHLFRGGTFYQLSNTRYRMALGAARGLAFLH-NAQPQVIY 201
QY 398 RQIKASNILIDFPEAKVADEFLAKTA--SDTNTHSVTRVMGTGYLAPEYAAASKLTKES 456
Db 202 RQFKASNILIDSNYAKLSDFLGARDSPHGDNSHVTRVMGTGYAAPEYATIGLSLVKS 261
QY 457 DYVSEFWLLELITGRPPDANNVYVDSLSVDWARPLNLRASEGDFEGGLADAKMNGYD 516
Db 262 DYVSEFWLLELISGRADKKNQGVGEHNLVDWAPYL---TNKRLLRVMDPLQSQYS 318
QY 517 REMARMVCAACACVHRSARRRPMQSVRALE 549
Db 319 LTRALKIAYALDLCISIDAKSRPTMNEIVKTIME 351
RESULT 5
CR14_MAIZE
ID CR14_MAIZE STANDARD; PRI; 301 AA.
AC 024585;
DT 15-DEC-1998 (Rel. 37, Created)
DD 15-DEC-1998 (Rel. 37, Last sequence update)
DE 15-JUN-2002 (Rel. 41, Last annotation update)
GN Putative receptor protein kinase CRINKL14 precursor (EC 2.7.1.-).
OS Zea mays (Maize).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade;
OC Panicoideae; Andropogoneae; Zea.
OC NCBI_TaxID=4577;
OC [1]
OC SEQUENCE FROM N.A.
OC STRAIN=cv. B73;
OC MEDLINE=96355669; PubMed=8703079;
OC Becraft P.W., Stinaard P.S., McCarty D.R.;
OC "CRINKL14: A TNFR-like receptor kinase involved in maize epidermal
OC differentiation.";
OC Science 273:3406-1409(1996).
CC -!- FUNCTION: PUTATIVE RECEPTOR PROTEIN KINASE. COULD PLAY A ROLE IN A
CC DIFFERENTIATION SIGNAL. THE CRINKL14 (CR4) MUTATION AFFECTS LEAF
CC EPIDERMIS DIFFERENTIATION SUCH THAT CELL SIZE AND MORPHOLOGY ARE
CC ALTERED, AND SURFACE FUNCTIONS ARE COMPROMISED, ALLOWING GRAFT-
CC LIKE FUSIONS BETWEEN ORGANS.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- SIMILARITY: BELONGS TO THE SER/TNR FAMILY OF PROTEIN KINASES.
CC -!- SIMILARITY: CONTAINS 1 TNFR-CYS REPEAT.
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or send an email to license@isb-sib.ch).

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DR EMBL: J67422; AAB09771.1; -
DR Maizeda; 128723; -
DR InterPro: IPR000719; Euk_pkinase.
DR InterPro: IPR004040; STY_pkinase.
DR InterPro: IPR002290; Ser_thr_pkinase.
DR InterPro: IPR001368; TNFR_c6.
DR Pfam: PF00020; TNFR_c6; 1.
DR Pfam: PF00069; pkinase; 1.
DR ProDom: PD000001; Euk_pkinase; 1.
DR SMART: SM00221; STYK; 1.
DR SMART: SM00208; TNFR; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00652; TNFR_NGFR_1; FALSE_NEG.
DR PROSITE: PS00050; TNFR_NGFR_2; 1.
KW Receptor; Transferase; Serine/threonine-protein kinase; ATP-binding;
FT SIGNAL 1 24
FT CHAIN 25 901
FT STRAIN-1 24
FT STRAIN-2 25
FT DOMAIN 25 423
FT TRANSMEM 424 444
FT DOMAIN 445 901
FT DOMAIN 33 330
FT REPEAT 33 68
FT REPEAT 72 107
FT REPEAT 125 160
FT REPEAT 162 195
FT REPEAT 203 236
FT REPEAT 253 287
FT REPEAT 292 330
FT REPEAT 357 391
FT DOMAIN 505 712
FT NP_BIND 511 519
FT BINDING 533 533
FT ACT_SITE 634 634
FT ACT_SITE 901 AA; 97439 MW; 52F8481AC187E061 CRC64;
Query Match 17.5%; Score 605; DB 1; Length 901;
Best Local Similarity 37.2%; Pred. No. 2.3e-16;
Matches 145; Conservative 82; Mismatches 129; Indels 34; Gaps 11;
QY 263 FTYELARATNGFSEANLLQGGFGYVHKGVLPSPGKEVAVKOLKVGSG--QGEREFCAEV 320
Db 493 FSYEELEQAGGFSQDSQVKGSGFSCVFKILRGDTVAVKRAKASDVVKSSKEEFNEL 552
QY 321 EILSRVHRHLVSLGVCYIAGAKRLLYVEFPVNNLEHLHGEG---RPTMWSRLKIA 377
Db 553 DLLSLRNHALLNLLGYCEDGSESLVYEPMAHGLYQHLHGKDPNKLKRLNWARRYTIA 612
QY 378 LGSAGLSLYHEDCNFKIHRDIKASNILIDFEAKVADFLAKIA-SDTNTHVSTFVM 436
Db 613 VQARGIEYLHGACPPVIRHIDIKSSNIIIDEDHNAFVADFGLSILGPADSGTPLSLPA 672
QY 437 GTFGYLAPEYAAAGKLTKEKSDVFSFGVWVLELTGRRPVDANNVYVDDSLVDNARPLNR 496
Db 673 GTGLGLDPEYRHLTKSDVYSFGVWVLEILSLGKRAIDMQ--FEEGNIVEAWVPLI-- 728
QY 497 ASQGDPEGLADAKMNGYDREEMARVACAAACVRRHARRRPMQIVRALEGNVSL-- 534
Db 729 --KAGDIFAILDPVLPSPDLEALKTIASVACACVVRGDRSMQKVTYALEHALALL 786
QY 555 --SDLNEGRMP-----GQSNVYSYGGSTDYDSSQZNMEDMKFRXKMGALQGYNATGEYS 607
Db 787 GSPCIEQPILPTEWILGSSRMHVKVQMSQSNHSCSE-NE-----LADGEQIGG-YR 835

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QY 608 NPTSDYGLYPSGSSSEGGQTREMEMGKIKR 637
Db 836 APS--WITFPSTSSQRRKSSAEDIVGR 863

RESULT 6
CLVL_ARATH STANDARD; PR: 980 AA.
ID CLVL_ARATH Q9SYQ8; 004380; Q9LQT2;
DT 16-OCT-2001 (rel. 40, Created)
DT 16-OCT-2001 (rel. 40, Last sequence update)
DT 15-JUN-2002 (rel. 41, Last annotation update)
DE Receptor protein kinase CLAVATA precursor (EC 2.7.2.-).
GN CLVL OR ATLG575820 OR T4012.5.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Landsberg erecta;
RX MEDLINE=97304386; PubMed=9160749;
RA Clark S.E., Williams R.W., Meyerowitz E.M.;
RT "The CLAVATA gene encodes a putative receptor kinase that controls
shoot and floral meristem size in Arabidopsis.";
RL Cell 89:575-585(1997).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=99178804; PubMed=10080719;
RA Williams R.W., Clark S.E., Meyerowitz E.M.;
RT "Genetic and physical characterization of a region of Arabidopsis
chromosome 1 containing the CLAVATA gene.";
RL Plant Mol. Biol. 39:171-176(1999).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RX MEDLINE=21016719; PubMed=11130712;
RA Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Karl S.,
White O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y.,
Buehler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,
Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,
Dunn P., Etgu P., Feldblum T.V., Feng J.-D., Fong B., Fujii C.Y.,
Gill J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Huzar L.,
Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,
Kim C.J., Koc H.L., Kremenetskaia I., Kurtz D.B., Kwan A., Lam B.,
Langin-Hooper S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P.,
Lin X., Liu S.X., Liu Z.A., Luros J.S., Maiti R., Marzilli A.,
Militscher J., Miranda M., Nguyen M., Nierman W.C., Osborne B.I.,
Pai G., Peterson J., Pham P.K., Rizzo M., Rooney T., Rowley D.,
Sakano H., Salzberg S.L., Schwartz J.R., Shinn P., Southwick A.M.,
Sun H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D.,
Utterback T., Van Aken S., Vaysberg M., Vysotskaia V.S., Walker M.,
Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.;
RT "Sequence and analysis of chromosome 1 of the plant Arabidopsis
thaliana";
RL Nature 408:816-820(2000).
CC -!- FUNCTION: ACTS WITH CLV3 TO CONTROL THE BALANCE BETWEEN MERISTEM
CELL PROLIFERATION AND DIFFERENTIATION. MAY ACT WITH CLV3 AS A
LIGAND-RECEPTOR PAIR IN A SIGNAL TRANSDUCTION PATHWAY.
CC CC COORDINATING GROWTH BETWEEN ADJACENT MERISTEMATIC REGIONS.
CC -!- SUBUNIT: MULTIMER (POTENTIAL).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
CC -!- TISSUE SPECIFICITY: IN A CENTRAL REGION OF THE SHOOT AND IN EARLY
FLOWER MERISTEMS.
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC -!- SIMILARITY: CONTAINS 18 LEUCINE-RICH REPEATS (LRR).
CC
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 EXBL: M76647; AAA33000.1; ALT_TERM.
 DR InterPro: IPR001480; B_lectin.
 DR InterPro: IPR000719; Fnk_pkinase.
 DR InterPro: IPR003609; Fnk_app.
 DR InterPro: IPR004040; STY_pkinase.
 DR InterPro: IPR002290; Ser_thr_pkinase.
 DR InterPro: IPR000858; Slocus_glycop.
 DR Pfam: PF00069; pkinase; 1.
 DR Pfam: PF00354; S_locus_glycop; 1.
 DR Pfam: PF01453; Agglutinin; 1.
 DR ProDom: P0000001; Euk_pkinase; 1.
 DR SMART: SM00108; B_lectin; 1.
 DR SMART: SM00473; PAN_AP; 1.
 DR SMART: SM00421; STYK; 1.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
 DR PROSITE: PS00011; PROTEIN_KINASE_DOM; 1.
 KW Transferase: Serine/threonine-protein kinase; Signal; ATP-binding;
 KW Transmembrane; Receptor; Glycoprotein; Self-incompatibility.
 FT SIGNAL 1 32 POTENTIAL.
 FT CHAIN 33 849 PUTATIVE SERINE/THREONINE KINASE RECEPTOR.
 FT DOMAIN 33 446 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 447 466 POTENTIAL.
 FT DOMAIN 467 849 POTENTIAL.
 FT DOMAIN 528 779 CYTOPLASMIC (POTENTIAL).
 FT NP_BIND 534 542 ATP (BY SIMILARITY).
 FT BINDING 556 556 ATP (BY SIMILARITY).
 FT ACT_SITE 653 653 BY SIMILARITY.
 FT CARBOHYD 47 47 N-LINKED (GLCNAC...) (POTENTIAL).
 FT CARBOHYD 120 120 N-LINKED (GLCNAC...) (POTENTIAL).
 FT CARBOHYD 196 196 N-LINKED (GLCNAC...) (POTENTIAL).
 FT CARBOHYD 260 260 N-LINKED (GLCNAC...) (POTENTIAL).
 FT CARBOHYD 314 314 N-LINKED (GLCNAC...) (POTENTIAL).
 FT CARBOHYD 389 389 N-LINKED (GLCNAC...) (POTENTIAL).
 FT CARBOHYD 442 442 N-LINKED (GLCNAC...) (POTENTIAL).
 FT SEQUENCE 849 AA; 97231 MR; 7E156059EDDF4370 CRC64;
 Query Match 16.6%; Score 572; DB 1; Length 849;
 Best Local Similarity 32.3%; Pred. No. 3.6e-15;
 Matches 139; Conservative 83; Mismatches 119; Indels 90; Gaps 11;
 QY 135 STGVVVGIAIGVALLIVITLCLCKKKRRDEEDAYVPPPPGPKAGGPGGQQQ 194
 DB 443 ASGKIISLTV-GVSVLLILMFC-LWKKOKKAKASAIAN----- 482
 QY 195 WRQONATPPSDHVTISLPPPKAPSPPPPPPPPPPPPPPPPPPPPPPPPP 254
 DB 483 -TQNQLPMNEVLS----- 497
 QY 255 VGFSGKSTP-----YEEL-----ARATNGFSEANLGGGYYHKGVLPSGKEY 300
 DB 498 ----SKREFSGYKFEELPLTETMETVVKATENESSCKLGQGGGIVYKGLLDGKEI 553
 QY 301 AVKQLKVGSGQGEREQAEVELISRVHHRHLSVGYCTAGAKRLVYFVPPNNLEHL 360
 DB 554 AVKRLSKTSVQGTDFEMFNFTLIARQHLNVLVGGCCTEGDEKMLYFTEENLSDSYL 613
 QY 361 HGEGRPT-NEWSTRKIALSGKLSYLEDNCPKLIHRDIKASNLIDFKEAKVADFG 419
 DB 614 FGKTRSKLWNERDITNGVARGLLYLHQDSRFRIIHRDLKVSNNLLDKNIPKISDFG 673
 QY 420 LAKIASDTNTHVST-RVMGTGYLAPEYAAAGKLTSEKSDVFSFGVWVLELITGRFPYDAN 478
 DB 674 MARIFERDETANTMKVGVGYGYSPEYAMYGIFSEKSDVFSFGVIVLVISVSKKNGRY 733
 QY 479 NYVVDLSVD--WAPLLNKASEQDGEGLADAKNNG--YDREMARVACAAACVRHS 534
 DB 734 NLIDYENDLLSVYWRKWEGRALIEVD-FVIVDSLSQSFIFQPEYKLCIQIGLLCVQEL 792

QY 535 ARRRPRMSQIV 545
 DB 793 AEHRPAMSSVV 803
 RESULT 8
 RLK5_ARATH STANDARD; PRT; 999 AA.
 AC P47735;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Receptor-like protein kinase 5 precursor (EC 2.7.1.-).
 GN RK5 OR A7428490 OR F2109.180.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC eudicotyledons; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
 OC NCBI_taxid=3702;
 [1]
 RN SEQUENCE FROM N.A.
 RP STRAIN=cv. Columbia;
 RX MEDLINE=94035150; PubMed=8220453;
 RA Walker J.C.;
 RA "Receptor-like protein kinase genes of Arabidopsis thaliana";
 Plant J. 3:451-456(1993).
 [2]
 RN SEQUENCE FROM N.A.
 RP STRAIN=cv. Columbia;
 RX MEDLINE=20083488; PubMed=10617198;
 RA Meyer X.F.X.; Schueller C.; Wambuit R.; Murphy G.; Volckaert G.;
 RA Pohl T.; Duesterhoeft A.; Stiekema W.; Entian K.-D.; Terryn N.;
 RA Harris B.; Ansorge W.; Brandt P.; Grivell L.A.; Rieger M.;
 RA Weichselgartner M.; de Simone V.; Obermaier B.; Mache R.; Mueller M.;
 RA Kreis M.; Delseny M.; Puigdomenech P.; Watson M.; Schmidheini T.;
 RA Reichert B.; Portetelle D.; Perez-Alonso M.; Boutry M.; Bancroft I.;
 RA Vos P.; Hohenseil J.; Zimmermann W.; Wedler H.; Ridley P.;
 RA Langham S.-A.; McCullagh B.; Billam L.; Robben J.;
 RA Van der Schueren J.; Grymonprez B.; Chuang Y.-J.; Vandenbussche F.;
 RA Braeken M.; Weltjens I.; Voet M.; Bastiaens I.; Aert R.; Defoor E.;
 RA Weitzenecker T.; Bothe G.; Ramsperger U.; Hilbert H.; Braun M.;
 RA Holzer E.; Brandt A.; Peters S.; van Staveren M.; Dirkse W.;
 RA Mooijman P.; Klein Lankhorst R.; Rose M.; Kauf J.; Koetter P.;
 RA Berner S.; Hempel S.; Feldpausch M.; Lamberth S.; van den Daele H.;
 RA De Keyser A.; Buyschaert C.; Gieles J.; Villarroel R.; De Clercq R.;
 RA Van Montagu M.; Rogers J.; Cronin A.; Quail M.; Bray-Allen S.;
 RA Clark L.; Doggett J.; Hall S.; Kay M.; Lennard N.; McLay K.; Mayes R.;
 RA Pettitt A.; Rajandream M.A.; Lyne M.; Benes V.; Rechmann S.;
 RA Borkova D.; Bloeker H.; Scharfe M.; Grimm M.; Loehnert T.-H.;
 RA Dose S.; de Haan M.; Maarse A.C.; Schaefer M.; Mueller-Auer S.;
 RA Gabel C.; Fuchs M.; Farman S.; Grandjean K.; Dauner D.; Herzl A.;
 RA Neumann S.; Argiriou A.; Vitale D.; Liguori R.; Piravandi E.;
 RA Massenet O.; Quigley F.; Clabaud G.; Kuendlin A.; Felber R.;
 RA Schnabl S.; Hiller R.; Schmidt W.; Lecharny A.; Aubourg S.;
 RA Chedor F.; Cooke R.; Berger C.; Monfort A.; Casacuberta E.;
 RA Gibbons T.; Weber N.; Vandenbol M.; Barges M.; Terol J.; Torres A.;
 RA Perez-Perez A.; Purnelle B.; Bent E.; Johnson S.; Tacon D.; Jesse T.;
 RA Heijnen L.; Schwarz S.; Scholler P.; Heber S.; Francis P.; Bielke C.;
 RA Frishman D.; Haase D.; Lemcke K.; Mewes H.-W.; Stocker S.;
 RA Zaccaria P.; Bevan M.; Wilson R.K.; de la Bastide M.; Habermann K.;
 RA Parnell L.; Dedhia N.; Gnoj L.; Schutz K.; Huang E.; Spiegel L.;
 RA Sekhon M.; Murray J.; Sheet P.; Cordes M.; Abu-Threideh J.;
 RA Stoneking T.; Kallio J.; Graves T.; Harmon G.; Edwards J.;
 RA Latreille P.; Courtney L.; Cloud J.; Abbott A.; Scott K.; Johnson D.;
 RA Minx P.; Bentley D.; Fulton B.; Miller N.; Greco T.; Kemp K.;
 RA Kramer J.; Fullon L.; Mardis E.; Dante M.; Pepin K.; Hillier L.;
 RA Nelson J.; Spieth J.; Ryan E.; Andrews S.; Geisel C.; Layman D.;
 RA Du H.; Ali J.; Berghoff A.; Jones K.; Drone K.; Cotton M.; Joshua C.;
 RA Antoniou B.; Zidanic M.; Strong C.; Sun H.; Lamar B.; Yordan C.;
 RA Ma P.; Zhong J.; Preston R.; Vil D.; Shekher M.; Matero A.; Shah R.;
 RA Swaby I.K.; O'Shaughnessy A.; Rodriguez M.; Hoffman J.; Zill S.;
 RA Granat S.; Shohdy N.; Hasegawa A.; Hameed A.; Lodhi M.; Johnson A.;

| | |
|--|---|
| DR | PRINTS; PR01217; PRTCHEXTENSN. |
| DR | PRINTS; PR01218; PSTLEXTENSIN. |
| KW | Glycoprotein; Repeat; Signal. |
| FT | SIGNAL 1 29 POTENTIAL. |
| FT | CHAIN 30 555 VEGETATIVE CELL WALL PROTEIN GP1. |
| FT | DOMAIN 40 339 '49 X 5 AA APPROXIMATE PPSPX REPEATS. |
| FT | DOMAIN 259 279 POLY-PRO. |
| FT | CARBOHYD 399 399 N-LINKED (GLCNAC. .) (POTENTIAL). |
| FT | CARBOHYD 455 455 N-LINKED (GLCNAC. .) (POTENTIAL). |
| FT | CARBOHYD 493 493 N-LINKED (GLCNAC. .) (POTENTIAL). |
| SC | SEQUENCE 555 AA; 54219 MW; 6A584A90465502F5 CRC64; |
| Query Match 12.6%; Score 434; DB 1; Length 555; Best Local Similarity 36.9%; Ered.No. 3.4e-10; Matches 103; Conservative 15; Mismatches 83; Indels 78; Gaps 10 | |
| QY | 5 PSPGTGS--PPSPPSNSTTIIPASAPPPPTTPSSPPPSTIPTSPSSRSTWPSAP--- 59 : : |
| Dd | 66 PSPPGPPAPPSPSPAPPSPAPTSPZAPPSPAPPSPAPPSPAPPSPAPPSPAPPSPPA 125 : : |
| QY | 60 -----PPSPPTSPFGSDPPL-----POPSEPATTGSP-----PAP--VTPPTRNPP- 101 |
| Dd | 126 PPSPPFPAPPSPSPAPPAPLPFPSPAPSPSPVPVPSPPVPPSPAPPSTPTTSPSPSPV 185 |
| QY | 102 ----PSPVGPPSPNSREGGSRP--PSPSPSPSSDGLSGVVGVGAIGVALIVTV 154 |
| Dd | 186 PPSAPPSPAPPVPPSPAPPSPAPPVPPSPAPPSPSPA----- 224 |
| QY | 155 LICLLKKRRDEDAYYVPPPPPGPKAGGYGGQQQWRQNATPPSHHVVTSLPPP 214 |
| Dd | 225 -----PPSPSPAPPSPSPA-----PPSPVPSPAPPSPAPPSP 258 |
| QY | 215 PKAPSPPRQP-PPPPPPPEMSSSGSDXSDEPVLPPSP 252 |
| Dd | 259 PKPPAPPSPSPPPPPPPPPRPFPFANIAPPSPPPSPSP 297 |
| RESULT 13 | |
| ID | TMLL ARATH STANDARD; PRT; 674 AA. |
| RC | P33543; |
| DT | 01-FEB-1994 (Rel. 23, Created) |
| DT | 01-FEB-1994 (Rel. 23, last sequence update) |
| DE | 15-JUN-2002 (Rel. 41, last annotation update) |
| DE | Putative kinase-like protein TMLL precursor. |
| GN | TKML1 OR AT3C24660 OR MSD24.3. |
| OS | Arabidopsis thaliana (Mouse-ear cress). |
| OC | Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; |
| OC | Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; |
| OX | eurosid II; Brassicales; Brassicaceae; Arabidopsi. |
| ON | NCB1_TaxID=3702; |
| [1] | SEQUENCE FROM N.A. |
| RP | STRAIN=cv. Columbia; TISSUE=Green siliques; |
| RC | MEDLINE=94033320; PubMed=8219075; |
| RX | Valon C., Smalle J., Goodman H.M., Giraudat J.; |
| RT | "Characterization of an Arabidopsis thaliana gene (TMLL) encoding a |
| RT | putative transmembrane protein; with an unusual kinase-like domain."; |
| RL | Plant Mol. Biol. 23:415-421(1993). |
| [2] | SEQUENCE FROM N.A. |
| RP | STRAIN=cv. Columbia; |
| RC | MEDLINE=20363099; PubMed=10907853; |
| RX | Kaneko T., Katoh T., Sato S., Nakamura A., Asamizu E., Tabata S.; |
| RA | "Structural analysis of Arabidopsis thaliana chromosome 3. II. |
| RT | Sequence features of the 4,251,695 bp regions covered by 90 Pl, TAC |
| RT | and BAC clones."; |
| RL | ENA Res. 7:217-221(2000). |
| CC | -!- SUBCELLULAR LOCATION: Type I membrane protein. |
| CC | -!- SIMILARITY: TO PROTEIN KINASES IN THE C-TERMINUS. BUT DOES NOT |
| CC | SEEM TO HAVE CONSERVED A KINASE ACTIVITY. |
| CC | -!- SIMILARITY: CONTAINS 7 LEUCINE-RICH REPEATS (LRR). |

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RESULT 12
GPI_CHLRE
ID GPI_CHLRE STANDARD; PRT; 555 AA.
AC Q9FP06; Q03927;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Vegetative cell wall protein gpl precursor (Hydroxyproline-rich
DE glycoprotein 1).
DE GN Gpi1.
OS Chlamydomonas reinhardtii.
OC Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
OC Chlamydomonadaceae; Chlamydomonas.
NCBI_TaxID=3055;
RN [1]
RN [2]
SEQUENCE FROM N.A.
MEDLINE=21159092; PubMed=11258910;
Ferris P.J., Woessner J.P., Waffenschmidt S., Kilz S., Drees J.,
Goodenough U.W.;
"Glucosylated polyproline II rods-with-kinks as a structural motif in
plant hydroxyproline-rich glycoproteins.";
Biochemistry 40:2978-2987(2001).
[2]
PARTIAL PRELIMINARY SEQUENCE FROM N.A.
MEDLINE=91017504; PubMed=16992225;
Adair W.S., Apt K.E.;
"Cell wall regeneration in Chlamydomonas: accumulation of mRNAs
encoding cell wall hydroxyproline-rich glycoproteins.";
Proc. Natl. Acad. Sci. U.S.A. 87:7355-7359(1990).
-!- FUNCTION: Major component of the outer cell wall W6 (crystalline)
layer.
-!- SUBUNIT: Associates with GP2 and GP3.
-!- PTM: N-glycosylated and O-glycosylated.
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EMBL; AF309494; AAG45420.1; -.
EMBL; M58496; AAA69706.1; ALT_SEQ.
GlycoSuiteDB; Q9FP06; -.
InterPro; IPR002965; P-rich_extensin.
InterPro; IPR003882; Pistil_extensin.

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366  ---PTMEWSTRKALGSAKGLSYLHEDCNPKIIRHDIKASNKILIDFKFAKVADFGLA 421
369  QNPLPALTWOORFSLSGTARGIYFLHTARGPLIHGDIKAPKANHLLDCLQPKIGDFGV 368
422  K---IASDNTNTHVSTRVNGTGYGLAPEYAAAGKLTESKDSVFGVVELELITGRPPVDAN 478
369  REGPKSLDAVVEVN-KVEGTIKYLPPEFRNFQSLSTGVDTVSFGVILLEVFTGRQVTD-- 425
479  NVYVDDSLVDHRRPLLNRASQGDDEGLAD-AKMNNGVYDREMAR-----MVA 525
426  -----RVPENETKNLLIDYVKQOWRQNRVLELKHAAAPMGKELDMCM 468
526  CAAA---CYRHSARRRPMISOIVRALE 549
469  CATCAGLHCTALDDQDRPSMNAVLRKE 496

RESULT 15
ID EXTN_TOBAC STANDARD; PRT; 620 AA.
AC PI3983;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DE 16-OCT-2001 (Rel. 40, Last annotation update)
DE Extension precursor (Cell wall hydroxyproline-rich glycoprotein).
GN HRPGN3.
OS Nicotiana tabacum (Common tobacco).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana.
ON NCBI_TaxID=4097;
RX [1]
RY SEQUENCE FROM N.A.
RP STRAIN=cv. Xanthi; TISSUE=Leaf;
RX MEDLINE=90128263; PubMed=2512909;
RT Keller B., Lamb C.J.;
RT "Specific expression of a novel cell wall hydroxyproline-rich
RT glycoprotein gene in lateral root initiation.";
RT Genes Dev. 3:1639-1646(1989).
RL CC
RL FUNCTION: HAS A SPECIALIZED STRUCTURAL FUNCTION, POSSIBLY IN
RL THE MECHANICAL PENETRATION OF THE CORTEX AND EPIDERMIS OF THE
RL MAIN ROOT.
CC CC
CC !- SUBCELLULAR LOCATION: Extracellular matrix.
CC !- PTM: EXTENSIONS CONTAIN A CHARACTERISTIC REPEAT OF THE PENTAPEPTIDE
CC SER-PRO(4). THE PROLINE RESIDUE IS HYDROXYLATED AND THEN
CC GLYCOSYLATED.
CC CC
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CC or send an email to license@isb-sib.ch).
CC CC
CC EMBL; X13885; CAA320390.1; -.
CC PIR; S06733; S06733.
CC Repeat; Cell wall; Glycoprotein; Signal; Structural protein;
CC Hydroxylation.
CC SIGNAL 1 20 POTENTIAL.
CC CHAIN 21 620 EXTENSION.
CC REPEAT 70 73 H-A-P-P.
CC REPEAT 148 151 H-A-P-P.
CC DOMAIN 229 242 2 X 7 AA TANDEM REPEATS OF T-H-R-H-A-P-P.
CC REPEAT 229 235 1.
CC REPEAT 236 242 2.
CC DOMAIN 205 520 CONTAINS THE SER-PRO(4) REPEATS.
CC DOMAIN 499 600 3 X APPROXIMATE TANDEM REPEATS.
CC SEQUENCE 620 AA; 65406 MW; 641DD2278AB28524 CRC64;

Query Match 10.4%; Score 360; DB 1; Length 620;
Matches 97; Conservative 9; Mismatches 65; Indels 94; Gaps 14;

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QY 4 APSGCTGSPSPSPNSNTTTPPPASAPPZTTTSSPPPTTIPTSPSSSRSTPSAPP-S 62
Db :||| ||| ||| :||| ||| ||| ||| ||| ||| :||| ||| |||
347 SPPPPVTSPPPPSPS-----PPPTYLPPPPSSPPPSFSP--PPPTYEQSPPPPAY 400
QY 63 PPTSTGSPPLPQSPSPATTTGSPAPVTPTRNPPSVPGPPSNPSREGGSPRPPS 122
Db ||| :||| ||| ||| ||| ||| ||| ||| ||| ||| :||| ||| |||
401 PPLPAPPTYSPPPPTYSPPPTYAQPPP---LPPTYSPPPPAYSPPPPTTY---SPPPPT 454
QY 123 -SPSPSPSSDGLSTGVVVGIAIGVALLVIVILCLLCKKKRRRDEEDAYVPPPP-- 179
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
455 YSPPPP-----AYAQPPPPPPPT 471
QY 180 --PGKAGGPGGQQQOMQQONATPPSDHVVTSLPPPKAPSPR-QPPPP-----Pppp 231
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
472 YSPPPPAYSP-----PPSP--IYSPPPQVQLPPTSPPPPRRHLPPPP 516
QY 232 FMSSSGSDYSDRPVLP-----PSP 252
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
517 HR-----QRPPTPTYGQPPSP 533
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Search completed: July 2, 2003, 15:22:46
Job time : 28 secs

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QM protein - protein search, using sw model

Run on: July 2, 2003, 15:16:13 ; Search time 73 Seconds
(without alignments)
1181.002 Million cell updates/sec

Title: US-10-086-464-2

Perfect score: 3453

Sequence: 1 MSAPSPGPGSPSPSPNST.....REMEMGKIKRTGGYSGPSL 647

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A_Geneseq_101002:*

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| 2: | /SID22/gcgdata/geneseq/geneseq-emb1/AA1981.DAT:* |
| 3: | /SID22/gcgdata/geneseq/geneseq-emb1/AA1982.DAT:* |
| 4: | /SID22/gcgdata/geneseq/geneseq-emb1/AA1983.DAT:* |
| 5: | /SID22/gcgdata/geneseq/geneseq-emb1/AA1984.DAT:* |
| 6: | /SID22/gcgdata/geneseq/geneseq-emb1/AA1985.DAT:* |
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| 8: | /SID22/gcgdata/geneseq/geneseq-emb1/AA1987.DAT:* |
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| 23: | /SID22/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:* |

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|--------|-------------|--------|----|--------------------|
| 1 | 344.0 | 99.6 | 647 | 22 | Brassica napus PER |
| 2 | 2936.5 | 85.0 | 652 | 23 | Arabidopsis thalia |
| 3 | 2260.5 | 65.5 | 544 | 21 | Arabidopsis thalia |
| 4 | 2093.5 | 60.6 | 694 | 23 | Arabidopsis thalia |
| 5 | 1748.5 | 50.6 | 633 | 22 | Arabidopsis thalia |
| 6 | 1748.5 | 50.6 | 633 | 23 | Arabidopsis thalia |
| 7 | 1729 | 50.1 | 699 | 23 | Arabidopsis thalia |
| 8 | 1687 | 48.9 | 674 | 22 | Arabidopsis thalia |
| 9 | 1687 | 48.9 | 674 | 23 | Arabidopsis thalia |
| 10 | 1683.5 | 48.8 | 700 | 23 | Arabidopsis thalia |

| | | | | | |
|----|--------|------|------|----|--------------------|
| 11 | 1569.5 | 45.5 | 509 | 23 | Arabidopsis thalia |
| 12 | 1515.5 | 43.9 | 710 | 23 | Arabidopsis thalia |
| 13 | 1459.5 | 42.3 | 708 | 23 | Arabidopsis thalia |
| 14 | 1456 | 42.2 | 681 | 23 | Arabidopsis thalia |
| 15 | 1415.5 | 41.0 | 731 | 22 | Arabidopsis thalia |
| 16 | 1400.5 | 40.6 | 308 | 21 | Arabidopsis thalia |
| 17 | 1399 | 40.5 | 731 | 22 | Arabidopsis thalia |
| 18 | 1399 | 40.5 | 731 | 23 | Arabidopsis thalia |
| 19 | 1397 | 40.5 | 509 | 23 | Arabidopsis thalia |
| 20 | 1369.5 | 39.7 | 718 | 23 | Arabidopsis thalia |
| 21 | 1022 | 29.6 | 394 | 23 | Arabidopsis thalia |
| 22 | 816.5 | 23.6 | 707 | 23 | Arabidopsis thalia |
| 23 | 802 | 22.9 | 435 | 23 | Arabidopsis thalia |
| 24 | 791.5 | 22.9 | 753 | 23 | Arabidopsis thalia |
| 25 | 780.5 | 22.6 | 472 | 21 | Arabidopsis thalia |
| 26 | 780.5 | 22.6 | 472 | 23 | Arabidopsis thalia |
| 27 | 775.5 | 22.5 | 541 | 21 | Arabidopsis thalia |
| 28 | 774 | 22.4 | 676 | 23 | Arabidopsis thalia |
| 29 | 773 | 22.4 | 492 | 21 | Arabidopsis thalia |
| 30 | 773 | 22.4 | 492 | 23 | Arabidopsis thalia |
| 31 | 769.5 | 22.3 | 450 | 21 | Arabidopsis thalia |
| 32 | 769.5 | 22.3 | 450 | 23 | Arabidopsis thalia |
| 33 | 764 | 22.1 | 497 | 21 | Arabidopsis thalia |
| 34 | 759 | 22.0 | 492 | 23 | Arabidopsis thalia |
| 35 | 757 | 21.9 | 523 | 21 | Arabidopsis thalia |
| 36 | 757 | 21.9 | 523 | 23 | Arabidopsis thalia |
| 37 | 757 | 21.9 | 530 | 21 | Arabidopsis thalia |
| 38 | 757 | 21.9 | 591 | 23 | Arabidopsis thalia |
| 39 | 757 | 21.9 | 596 | 23 | Arabidopsis thalia |
| 40 | 757 | 21.9 | 610 | 21 | Arabidopsis thalia |
| 41 | 757 | 21.9 | 615 | 21 | Arabidopsis thalia |
| 42 | 754.5 | 21.9 | 968 | 21 | Arabidopsis thalia |
| 43 | 750 | 21.7 | 516 | 22 | Arabidopsis thalia |
| 44 | 745 | 21.6 | 1045 | 23 | Arabidopsis thalia |
| 45 | 744.5 | 21.6 | 456 | 21 | Arabidopsis thalia |

ALIGNMENTS

RESULT 1
AAB74205
ID AAB74205 standard; protein; 647 AA.
XX AAB74205;
XX AC
XX DT 17-MAY-2001 (first entry)
XX DE Brassica napus PERK1 protein.
XX KW Proline-rich extensin-like receptor kinase; PERK; resistance;
XX plant.
XX OS Brassica napus.
XX PN WO200114563-A1.
XX PD 01-MAR-2001.
XX PF 18-AUG-2000; 2000WO-CA00966.
XX PR 19-AUG-1999; 99US-0149466.
XX PR 13-OCT-1999; 99US-0159122.
XX {GORI/} GORING D.
XX {SILV/} SILVA N.
XX Goring D, Silva N;
XX WPI; 2001-244305/25.
XX New proline-rich, extensin-like receptor kinase nucleic acids and
XX polypeptides useful for increasing plant wounding or pathogen

PT resistance, or for producing transgenic plants with increased wounding
 PT or pathogen resistance
 XX Claim 30; Fig 1; 91pp; English.
 XX The present invention relates to proline-rich extensin-like
 CC receptor kinase (PERK). The PERK nucleic acids and polypeptides
 CC are useful for increasing the resistance of plants to wounding
 CC and pathogens. These are also useful for producing transgenic
 CC plants with increased wounding and pathogen resistance compared
 CC with a wild type plant, as well as in assays for identifying
 CC and developing compounds to inhibit and/or enhance polypeptide
 CC function directly.
 XX Sequence 647 AA;
 SQ

Query Match 99.6%; Score 3440; DB 22; Length 647;
 Best Local Similarity 99.7%; Pred. No. 4e-181; 2; Indels 0; Gaps 0;
 Matches 645; Conservative 0; Mismatches 2;

QY 1 MSSAPSGTGGSPSPSTTTTPPPASAPPTTSSPPPTTPTSSPPPTTPTSSPPSTPSAPP 60
 DB 1 MSSAPSGTGGSPSPSTTTTPPPASAPPTTSSPPPTTPTSSPPPTTPTSSPPSTPSAPP 60
 QY 61 PSPPTSPGSPPLPQSPAPPTTGGSPAPPTTTPTRNPPSPVGPSPNREGSPRP 120
 DB 61 PSPPTSPGSPPLPQSPAPPTTGGSPAPPTTTPTRNPPSPVGPSPNREGSPRP 120
 QY 121 PSSPSPSPSSDGLSTGVVVGIAIGVALLVITLILCLLCKKKRRRDEDAVYVPPPPP 180
 DB 121 PSSPSPSPSSDGLSTGVVVGIAIGVALLVITLILCLLCKKKRRRDEDAVYVPPPPP 180
 QY 181 GKAGGPGGQOQWROQNAATPPSDHYVTSLPPPKAPSPRPPPPPPPMSSGGSD 240
 DB 181 GKAGGPGGQOQWROQNAATPPSDHYVTSLPPPKAPSPRPPPPPPPMSSGGSD 240
 QY 241 YSDRPVLPSPSPGLVGFSGKSTFTYEELARATNGFSEANLILQGGGFGVHGVLPSGKEV 300
 DB 241 YSDRPVLPSPSPGLVGFSGKSTFTYEELARATNGFSEANLILQGGGFGVHGVLPSGKEV 300
 QY 301 AVKOLKVGSGGGEREFQAEVEIISRVHRRHLVSLVGYCIAGAKRLLYVEFPNNLELHL 360
 DB 301 AVKOLKVGSGGGEREFQAEVEIISRVHRRHLVSLVGYCIAGAKRLLYVEFPNNLELHL 360
 QY 361 HGEGRPTMEWSTRUKIALGSAKGLSYLHEDCNPKIIRHDIKASNLIDFKFAKVADFG 420
 DB 361 HGEGRPTMEWSTRUKIALGSAKGLSYLHEDCNPKIIRHDIKASNLIDFKFAKVADFG 420
 QY 421 AKIASDTNTHVSTRVMTGTFGLAPEYAAAGSKLTEKSDVFSFGVLLLEITGRRPVDA 480
 DB 421 AKIASDTNTHVSTRVMTGTFGLAPEYAAAGSKLTEKSDVFSFGVLLLEITGRRPVDA 480
 QY 481 YVDSLVDMARPLNLRASGQDFEGLADAKNNNGYDREEMARVACAAACVRRSARRPR 540
 DB 481 YVDSLVDMARPLNLRASGQDFEGLADAKNNNGYDREEMARVACAAACVRRSARRPR 540
 QY 541 MSQIVRALEGNVSLDLNEMRGQSNVSYSGGSTDYDSQYEDMKTKRMALGQY 600
 DB 541 MSQIVRALEGNVSLDLNEMRGQSNVSYSGGSTDYDSQYEDMKTKRMALGQY 600
 QY 601 NATGEYSNPTSDYGLYPSGSSSGQTTREMEMKIKETGOGYSGPSL 647
 DB 601 NATGEYSNPTSDYGLYPSGSSSGQTTREMEMKIKETGOGYSGPSL 647

RESULT 2
 ID ABB92424
 XX ABB92424 standard; Protein; 652 AA.
 AC ABB92424;
 XX
 DT 31-MAY-2002 (first entry)
 XX

Herbicidally active polypeptide SEQ ID NO 1635.
 Herbicidal; plant; agriculture; herbicide.
 Arabidopsis thaliana.
 WO200210210-A2.
 07-FEB-2002.
 28-AUG-2001; 2001WO-EP09892.
 28-AUG-2001; 2001WO-EP09892.
 (FARB) BAYER AG.
 Tietjen K, Weidler M;
 WPI; 2002-269010/31.
 Identifying plant target proteins for herbicidally active compounds,
 comprising aligning and comparing nucleic acid or amino acid sequences
 from plant with nucleic acid or amino acid sequences from non-plant
 organisms -
 Claim 5; SEQ ID NO 1635; 261pp + Sequence Listing; English.
 The invention relates to identifying target proteins
 (ABB92730-ABB94016) for herbicidally active compounds, comprising
 aligning and comparing nucleic acid or amino acid sequences from plant
 with nucleic acid or amino acid sequences from non-plant organisms using
 suitable search parameters, where plant sequences having an E-value
 greater by a factor of 3 than the E-value of most similar non-plant
 sequences are selected. The polypeptides or nucleic acids encoding them
 are useful for identifying modulators. The identified modulators are
 useful as herbicides.
 Sequence 652 AA;
 Query Match 85.0%; Score 2936.5; DB 23; Length 652;
 Best Local Similarity 87.0%; Pred. No. 1.7e-153;
 Matches 574; Conservative 24; Mismatches 41; Indels 21; Gaps 12;

QY 1 MSSAPSGT--GSPSPSPSTTTTPPPA--SAPPTTSPSPPP--PSTTTPSPSPSSKS 54
 DB 1 MSTAPSGTTPSPSPSTTTTPPPAASSPPPTTTPSPSPSTSTSTSPSPSP 60
 QY 55 TPSAPPPPTTTPSPSPPLPQSPAPPTTTPSPAPVTPPT--RNPPSPVGPSPNPSR 113
 DB 61 PPS--PPSPSGSLT---PPLPQSPAPITP--SPSPSTTSPNPSRSPSPNPGPTPS- 114
 QY 114 EGGSPRPSS--PSPSPSSDGLSTGVVVGIAIGVALLVITLILCLLCKKKRRR--DEE 169
 DB 115 -GSTPTSPNTKPSPPSPSDGLSTGVVVGIAIGVALLVITLILCLLCKKKRRHDE 173
 QY 170 DAYVVPSPPPPGKAGGPGGQOQWROQNAATPPSD--HVVISLPPPKAPSPQPPPPP 228
 DB 174 AAYVVPSPPPPGKAGGPGGQOQWROQNAASPDNEHVTS--L--PPPKPPSPPKPPPPP 232
 QY 229 PPP--FMSSSGSDYSDRPVLPSPSPGLVGFSGKSTFTYEELARATNGFSEANLILQGGGFG 287
 DB 233 PPPAFMSSSGSDYSDLPVLPSPSPGLVGFSGKSTFTYEELARATNGFSEANLILQGGGFG 292
 QY 288 YVHGVLPSPKEVAVKOLKVGSGGGEREFQAEVEIISRVHRRHLVSLVGYCIAGAKRLV 347
 DB 293 YVHGVLPSPKEVAVKOLKVGSGGGEREFQAEVEIISRVHRRHLVSLVGYCMAGVQLV 352
 QY 348 YEVVNNNLEHLHGEGRPTMEWSTRUKIALGSAKGLSYLHEDCNPKIIRHDIKASNL 407
 DB 353 YEVVNNNLEHLHGEGRPTMEWSTRUKIALGSAKGLSYLHEDCNPKIIRHDIKASNL 412
 QY 408 DEFKEARVADFGIAGLAKIASDTNTHVSTRVMTGTFGLAPEYAAAGSKLTEKSDVFSFGVLL 467

Db 413 DFKEAKVADFGLAKIASDINTHVSTRVMGTGFLAPEYAAAGKLTESDVFSGVVILLE 472
QY 468 LITGRPVDANNVYDDSLVDNARPELLNRSASQGDPEGLADAKMNGYDREEMARVACA 527
Db 473 LITGRPVDANNVYDDSLVDNARPELLNRSASQGDPEGLADAKMNGYDREEMARVACA 532
QY 528 AACVRSARRPRMSOIVRALEGNVSLDLNEGMRPQSNVTSYSGSIDYDSSQYNEDM 587
Db 533 AACVRSARRPRMSOIVRALEGNVSLDLNEGMRPQSNVTSYSGSIDYDSSQYNEDM 592
QY 588 KFERKALQTYEATGYSNPTSDYGLYPSGSSSEGTREMEMCKIKRTGOGYSGPSL 647
Db 593 IKFERKALQTYEATGYSNPTSDYGLYPSGSSSEGTREMEMCKIKRTGOGYSGPSL 652

RESULT 3
AAG15453
ID AAG15453 standard; Protein; 544 AA.
XX AC AAG15453;
DT 17-OCT-2000 (first entry)
XX DE Arabidopsis thaliana protein fragment SEQ ID NO: 15711.
KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
OS Arabidopsis thaliana.
XX PN EP1033405-A2.
XX PD 06-SEP-2000.
XX PF 25-FEB-2000; 2000EP-030439.
XX 25-FEB-1999; 99US-0121825.
PR 05-MAR-1999; 99US-0123180.
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PR 23-MAR-1999; 99US-0123788.
PR 25-MAR-1999; 99US-0126264.
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PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

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Query Match

65.5%; Score 2260.5; DB 21; Length 544;

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Best Local Similarity 83.3%; Pred. No. 1.8e-116;
Matches 449; Conservative 27; Mismatches 40; Indels 23; Gaps 14;

QY 1 MSSAPSGT---GSPSPPSNSITTTTPPA--SAPPTTTPSSPP--PSTTTPSPSSRS 54
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Db 1 MSTAPSGTTPSPSPPTNSITTTTPPAASPPPTTTPSSPPPSFSTNSTSPSPSPL 60
  ||:||||| |||||:||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 55 TPSAPSPPTTPSPSPPLPOSPAPPTTPSPAPPTTP--RNPPSPVGGPPSPSR 113
  ||:||||| |||||:||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 51 PPSLPPSPSPGSLT---PPLQPSAPITP--SPSPPTPSNPSPPSPNOGPPNPS- 114
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QY 114 EGSPSPSPS--PSPSPSSDGLSTGVVGIATGGVALLVILICLLCKKKRR--DEE 169
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Db 115 -GSIPRTPSNAKSPSPSSDGLSTGVVGIATGGVALLVILICLLCKKKRRHDE 173
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QY 170 DAYVPPPPPPGKAGPYGGQQOQNRQONATPESD--HYVTSLPPPPKAPSPRQPPPP 228
  |||| |||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 174 AAYTV-PPPPSGPKAGPYGGQQOQYWOQONASPSDNHVTSL-PPPKPSPPKPPPP 231
  |||| |||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 229 PPP-EMSSSGSDYSDRPVLPSPSGVLGFSKSTTYEELARATNGFSANLLGGGFG 287
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Db 232 PPPAFMSSSGSDYSDLPVLPSPSGVLGFSKSTTYEELSRATNGFSANLLGGGFG 291
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QY 288 YVHKGYLPSGKEVAVKQKLVGSGQGEREFQAEVEIISRVHRHLVSLVGVCIAGAKRLV 347
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Db 292 YVHKGYLPSGKEVAVKQKLVGSGQGEREFQAEVEIISRVHRHLVSLVGVCIAGAKRLV 351
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QY 348 YEFVNNLEHLHGEGRTMEWSTRLKIALGSAKGLSYLHEDCNPKIHRD:KASNILI 407
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Db 352 YEFVNNLEFHLHGKGRPTMEWSTRLKIALGSAKGLSYLHEDCNPKIHRDIKASNILI 411
  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 408 DFKFEAKVADFGLAKIASDTNTHVSTRVMGTFCYLAPYAAAGSKLTKESDVSFGVLE 467
  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 412 DFKFEAKVADFGLAKIASDTNTHVSTRVMGTFCYLAPYAAAGSKLTKESDVSFGVLE 471
  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 468 LITGRPDANNVYDDSLVDWARPLNRSQDGEGLADAKMNGY--DREEMARWA 525
  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 472 LITGRPDANNVYDDSLVDWARPLNRSQDGEGLADAKMNGY--DREEMARWA 530
  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

```

RESULT 4

ABB92421

ID ABB92421 standard; Protein; 694 AA.

AC ABB92421;

XX ABB92421;

XX ABB92421;

DF 31-MAY-2002 (first entry)

DE Herbicidally active polypeptide SEQ ID NC 1632.

KW Herbicidal; plant; agriculture; herbicide.

OS Arabidopsis thaliana.

XX WO200210210-A2.

XX 07-FEB-2002.

XX 28-AUG-2001; 2001WO-EP09892.

XX 28-AUG-2001; 2001WO-EP09892.

XX {PAB } BAYER AG.

XX Tietjen K, Weidner M;

XX WPI; 2002-269010/31.

Identifying plant target proteins for herbicidally active compounds,
 comprising aligning and comparing nucleic acid or amino acid sequences
 from plant with nucleic acid or amino acid sequences from non-plant
 organisms -

XX

Db 348 IADGQRLVYEFVFNKILEYHLGKGLPVMFEFSTRIALGAAGKGLAYLHEDCHPRIIHR 407
 QY 399 DIKASNLIDFKFAKVADEGLAKIASDINTHVSTRVNGIFGYLAPEYAASGKLTESDV 458
 Db 406 DIKASNLIDFEDAMVADFGLAKLTSNDNTHVSTRVNGIFGYLAPEYAASGKLTESDV 467
 QY 459 FSFGVLELITGRPRVDANNVYDSDVADWARPLNRAASOGDFEGLADAKMNGYDRE 518
 Db 468 FSYGVMLELITGRPRVD-NSITMDTLDVWARPLMARALDGNFELADARLEGNYPQ 526
 QY 519 EMARWVACAAACVHRSARRPRMSQIVRALDGNVSLDNLNMGMRPGSQNVYSSXGSDY 578
 Db 527 EMARWVACAAASIRHSGKRKPKMSQIVRALEGEVSLDALNKGVPKPGHNVYSGLSADY 586
 QY 575 DSSQYNEDMKFKRMALGTQBY---NATGEYSNPTS DYG 614
 Db 587 SQTSYNADMKKFQIALSSQEFVSDCEGTSSNDSDRMG 625

RESULT 6

ID ABB91790 standard; Protein; 633 AA.
 AC ABB91790;

DI 31-MAY-2002 (first entry)

DE Herbicidally active polypeptide SEQ ID NO 1001.

KW Herbicidal; plant; agriculture; herbicide.

OS Arabidopsis thaliana.

PN WO200210210-A2.

PD 07-FEB-2002.

PF 28-AUG-2001; 2001WO-EPC9892.

PR 28-AUG-2001; 2001WO-EPC9892.

PA (FARB) BAYER AG.

PI Tietjen K, Weidler M;

DR WPI; 2002-269010/31.

XX Identifying plant target proteins for herbicidally active compounds,
 PT comprising aligning and comparing nucleic acid or amino acid sequences
 PT from plant with nucleic acid or amino acid sequences from non-plant
 XX organisms -

PS Claim 5; SEQ ID NO 1001; 261pp + Sequence Listing; English.

XX The invention relates to identifying target proteins
 CC (ABB90796-ABB94016) for herbicidally active compounds, comprising
 CC aligning and comparing nucleic acid or amino acid sequences from plant
 CC with nucleic acid or amino acid sequences from non-plant organisms using
 CC suitable search parameters, where plant sequences having an E-value
 CC greater by a factor of 3 than the E-value of most similar non-plant
 CC sequences are selected. The polypeptides or nucleic acids encoding them
 CC are useful for identifying modulators. The identified modulators are
 XX useful as herbicides.

SQ Sequence 633 AA;

Query Match 50.6%; Score 1748.5; DB 23; Length 633;

Best Local Similarity 56.8%; Pred. No. 2.5e-88;

Matches 363; Conservative 78; Mismatches 151; Indels 47; Gaps 15;

QY 3 SAPSPGTCGPPSPPSNTTTPPPASAPPTTPPSFPPPTTTPSPSSSRSTPPSAPPS 62
 Db 7 SAPPTNISTSPFSTNTSTSSP---PAPSPFTPTPFGDSSSSPPDPSTSPFAPQADN 63

QY 63 PPTPTSGPSPPLPQSPAPPTTPGSPAPVTPPTNPPSPVPGPSPNPSREGSPR--P 120
 Db 64 PPN-SSNNSPSPSQGGGGERGNGNGNDPPPSRGSPSPS---PFSRNGDNGGSRSP 119
 QY 121 PS-----SPSPSP--SSDG-----LSTGVVWGIAIGGVALLVIVTLICLCKKKR 165
 Db 120 PGDTGSRSDNPPSSGGSGGGGGRSNTNTAITVGLVAGGLMIVLIVCLRRKKKK 179
 QY 166 RDEEDAYVPPPPPPGPKAGP--YGGQQQWQONATPPSDHVVVISLPPPKAPSPR 222
 Db 180 ---DSFY-----PEPMKNGQYQYGNNNNNASONY--PMWHLNSQGNQOQSGWG 227
 QY 223 QPPPPPPPPSSSG--3SDYS--DRPVLPPSPGLVLGFSKSTTYIELARATNGFSEA 278
 Db 228 GGPSPPPPPRMTSGEDSSMYSGPSRPVLPSPALALGFKNSTTYQELAANTGGFTA 287
 QY 279 NLGGGEGYVHKVLPKSGEVAVKQLVKGSGGGERFQAEVEIISRVHHRHLVSLVGYC 338
 Db 288 NLLGGGEGYVHKVLPKSGEVAVKSLKAGSGGGERFQAEVDIISRVHHRVLSLVGYC 347
 QY 339 IAGAKRLVYEFVFPNNLELHLHGGRPTMEKSTRKIALGSAKGLSYLHEDCNPKIHR 398
 Db 348 IADGQRLVYEFVFNKILEYHLGKGLPVMFEFSTRIALGAAGKGLAYLHEDCHPRIIHR 407
 QY 399 DIKASNLIDFKFAKVADEGLAKIASDINTHVSTRVNGIFGYLAPEYAASGKLTESDV 458
 Db 408 DIKASNLIDFEDAMVADFGLAKLTSNDNTHVSTRVNGIFGYLAPEYAASGKLTESDV 467
 QY 459 FSFGVLELITGRPRVDANNVYDSDVADWARPLNRAASOGDFEGLADAKMNGYDRE 518
 Db 468 FSYGVMLELITGRPRVD-NSITMDTLDVWARPLMARALDGNFELADARLEGNYPQ 526
 QY 519 EMARWVACAAACVHRSARRPRMSQIVRALDGNVSLDNLNMGMRPGSQNVYSSXGSDY 578
 Db 527 EMARWVACAAASIRHSGKRKPKMSQIVRALEGEVSLDALNKGVPKPGHNVYSGLSADY 586
 QY 575 DSSQYNEDMKFKRMALGTQBY---NATGEYSNPTS DYG 614
 Db 587 SQTSYNADMKKFQIALSSQEFVSDCEGTSSNDSDRMG 625

RESULT 7

ID ABB91291 standard; Protein; 699 AA.
 AC ABB91291;

DT 31-MAY-2002 (first entry)

DE Herbicidally active polypeptide SEQ ID NO 502.

KW Herbicidal; plant; agriculture; herbicide.

OS Arabidopsis thaliana.

PN WO200210210-A2.

PD 07-FEB-2002.

PF 28-AUG-2001; 2001WO-EPC9892.

PR 28-AUG-2001; 2001WO-EPC9892.

PA (FARB) BAYER AG.

PI Tietjen K, Weidler M;

DR WPI; 2002-269010/31.

XX Identifying plant target proteins for herbicidally active compounds,
 PT comprising aligning and comparing nucleic acid or amino acid sequences
 PT from plant with nucleic acid or amino acid sequences from non-plant


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XX PN WO200210210-A2.
XX PD 07-FEB-2002.
XX PF 28-AUG-2001; 2001WO-EP09892.
XX PR 28-AUG-2001; 2001WO-EP09892.
XX PA (FARB ) BAYER AG.
XX PI Tietjen K, Weidler M;
XX PWPI; 2002-269010/31.
XX PT Identifying plant target proteins for herbicidally active compounds,
XX PT comprising aligning and comparing nucleic acid or amino acid sequences
XX PT from plant with nucleic acid or amino acid sequences from non-plant
XX PT organisms -
XX PS Claim 5; SEQ ID NO 715; 261pp + Sequence Listing; English.
XX PX
XX CC The invention relates to identifying target proteins
XX CC (ABB90790-ABB94016) for herbicidally active compounds, comprising
XX CC aligning and comparing nucleic acid or amino acid sequences from plant
XX CC with nucleic acid or amino acid sequences from non-plant organisms using
XX CC suitable search parameters, where plant sequences having an E-value
XX CC greater by a factor of 3 than the E-value of most similar non-plant
XX CC sequences are selected. The polypeptides or nucleic acids encoding them
XX CC are useful for identifying modulators. The identified modulators are
XX CC useful as herbicides.
XX CC
XX SQ Sequence 708 AA;

Query Match 42.3%; Score 1459.5; DB 23; Length 708;
Best Local Similarity 41.8%; Pred. No. 2e-72;
Matches 317; Conservative 90; Mismatches 127; Indels 225; Gaps 21;

QY 1 MSSAP-----SGETGSPSPSSNTT-TTPPASAP-PRTTP--SSPPPTTITSP 48
DB 1 MATTPQPVNSFPVTSPPPLNNATSPATPPVTSPLPPSAPPNRPAPPPPVTTSP 60
QY 49 PPSRSTP-----SAPPSPPTPTGSPPLPQP-----SPP---APTTP 86
DB 61 PPVANGAPPPLPKPPSSSPQPVIPSPSTSPQPVIPSPSPASDPPLALVPLP 120
QY 87 GSPAP-VTTP-----TNPPSV-----PQPSN-PSREGGSRPPSPS--- 124
DB 121 SSPPPPASVPPPPSPSPPLVRSPPSVRIQSPPPPSDRPTQSPPPSPSPSPSERP 180
QY 125 --SPPSPSDGLSTGVVVGIAIGVALLVITLCLCKKKRDEEDAYVPPPPGP 182
DB 181 TQSPSPSPS-----ERTQSPPPSPSP--- 202
QY 183 XAGGPGYGGQQQWROONATPPSDRVVTSLEPPPK--APSPRPQPPPPPPPPFMS----- 234
DB 203 -----SPPDRPQSPPPPEDTKPQPRSPNSPPTFSSPPSP 244
QY 235 -----SSGGSDYDRPVLPSP----- 250
DB 245 EILVPGSNPQSNQNTLRPLDAPNSTNSGIGTGAVVGISVAVLVFTLGFIVWCLR 304
QY 251 -----SPGLV-----LGFSKST 262
DB 305 KREKRLSAYSGGDVTFSPMSSTARSAPFRMOSAPVGAASKRSGSYQSGGIGNSKAL 364
QY 263 FTYEELARATNGFSEANLLGQGFYVHKGLVPSGKEVAVKQLKVGSGQGERFQAEVEI 322
DB 365 ESYEELVKATNGFSEANLLGEGFGCVYKILPDGRVAVKQLKIGGQGDREFFKAEVET 424
QY 323 ISKVHRLHLSVGYCIAGAKRLLYEVEPNNNLELHLHGEGRPTMEWSTRLKIALGSAK 382
DB 425 LSRIRHRLHLSVIGHCISGRDRLIYDYSNNDLYFELHGE-KSVLDWATRVKIAGAAR 483

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QY 383 GLSYLHEDCNPKLIHRDIKASNILIDPKFAKVADFGIAKIASDINTHVSTRMGTFFGL 442
DB 484 GLAYLHEDCHPRIIHRDIKSSNILEDFDARVDFGLARLALDONTHTITRVTIGTGM 543
QY 443 APEVAASGKLTSEKSDVSEFVGVVLLLTIGRRPVDANNVYDDSLVDWAPLNRASEQD 502
DB 544 APEYASSGKLTSEKSDVSEFVGVVLLLTIGRRPVDTSQPLGDESLVWARPLSHALETEE 603
QY 503 FEGLDAAKNNGYDREEMARKVACAAACVRSARRPRMSQIVRALEGNVLSLDLNEGMR 562
DB 604 FDSLADPKLGGNYVESEFMETIEAAGACVRLHATKPRMGQIVRAFE-SLAAEDLTNGMR 662
QY 563 PQSNVSYSGSDTDYDSSQYNEDMKKFKRMALGTOEYN 601
DB 663 LGESEV-----FNSAQOQSAEIRLFRMAFGSONYS 652

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RESULT 14

ABB93650
ID ABB93650 standard; Protein; 681 AA.

XX AC ABB93650;

XX DT 31-MAY-2002 (first entry)

XX DE Herbicidally active polypeptide SEQ ID NO 2861.

XX KW Herbicidal; plant; agriculture; herbicide.

XX OS Arabidopsis thaliana.

XX PN WO200210210-A2.

XX PD 07-FEB-2002.

XX PF 28-AUG-2001; 2001WO-EP09892.

XX PR 28-AUG-2001; 2001WO-EP09892.

XX PA (FARB) BAYER AG.

XX PI Tietjen K, Weidler M;

XX DR WPI; 2002-269010/31.

XX PT Identifying plant target proteins for herbicidally active compounds,
XX PT comprising aligning and comparing nucleic acid or amino acid sequences
XX PT from plant with nucleic acid or amino acid sequences from non-plant
XX PT organisms -

XX PS Claim 5; SEQ ID NO 2861; 261pp + Sequence Listing; English.

XX CC The invention relates to identifying target proteins
XX CC (ABB90790-ABB94016) for herbicidally active compounds, comprising
XX CC aligning and comparing nucleic acid or amino acid sequences from plant
XX CC with nucleic acid or amino acid sequences from non-plant organisms using
XX CC suitable search parameters, where plant sequences having an E-value
XX CC greater by a factor of 3 than the E-value of most similar non-plant
XX CC sequences are selected. The polypeptides or nucleic acids encoding them
XX CC are useful for identifying modulators. The identified modulators are
XX CC useful as herbicides.

XX SQ Sequence 681 AA;

Query Match 42.2%; Score 1456; DB 23; Length 681;

Best Local Similarity 46.4%; Pred. No. 3e-72; Indels 108; Gaps 14;

Matches 306; Conservative 87; Mismatches 158; Indels 108; Gaps 14;

QY 1 MSSAPSPGTSPPSPSPSNTTTTTPPASAPATPTTPSPSPPTTPTSPSPSRSTPSAPP 60

DB 52 VSSSPPPPVVSSP-PPSSSPSPSPVTSPPVTASSPPPVVATSPPTPATTPAPP 110

QY 51 -----PSPPTPSTGSP-----PPLPQPPPPAPTPTS 88
 Db 111 QTVSPPPDDASPPAPTINPKQSPSPGTPSPGTPSPKSPSPPTPTTIS 170
 QY 89 PPAP-----VTPPTNP-----PPSPGCP-----PSNPSREGGSPRPPSSPP 127
 Db 171 PPPPATASPPSPGNTDPSLAPPTPLPVYPRKPIAKPTGASNNGNLTPSS----- 226
 QY 128 SPSSDGLSTG--VVVGAIGGVALLVITLCLCKKKRRDEEDAYVPPPPPPKAG 185
 Db 227 SPKSEVGTGIVAIGVIGVLSFLVGVWFTKRAKDKDFTVGTMTMP-----SAYS 282
 QY 186 GPYGGQQQWQONATPPSDHVTSLPPPPKAPSPRPPPPPPPPPPSSSGGSDYSDRP 245
 Db 283 SPQSGDVVLENSRSAPPK-----MRSHSGSDY----- 310
 QY 246 VLPPPSGLVLFSGSKSTFTTEELARATNGFSEANLGGGFGYVHKGVLPKGVEAVKQL 305
 Db 311 MYASSDGMVSN-QRSWFSEYDELSQVTSFSEKNLGGGFGYVKGVLSDGREVAVKQL 369
 QY 305 KVGSGQGEREFQAEVEIISKVVHRLVSLVGYCIAGAKRLLVYEFVPPNNLELHLCGER 365
 Db 370 KIGSGQGEREFQAEVEIISKVVHRLVSLVGYCIAGAKRLLVYEFVPPNNLELHLCGER 429
 QY 366 PTMEWTRKIALGSAKGLSYLHEDCKPIIHRDIKASNILIDFKFAKVAFDGLAKIAS 425
 Db 430 PVMETWTRVRAAGAARGIAYLHEDCKPIIHRDIKSSNILLDSFALYADFLAKIAQ 489
 QY 426 --DNTHTVSRVMTGTYLAPEYAAKGLTEKSDVTFSGVVLLELITGRPPVDANNVYD 483
 Db 490 ELDLNTHTVSRVMTGTYLAPEYAAKGLTEKSDVTFSGVVLLELITGRPPVDANNVYD 549
 QY 484 DSLVDWARPPLNRASEOGDFEGLADAKNNNGYDREEMARVACAAACVRSARRPRMSQ 543
 Db 550 ESLVEMARPPLGQAIENEBEDELVDPLKKNFIPCEMFRVVEAAACVRSARRPRMSQ 609
 QY 544 IVRALEGNVSLDNEGMRPGQSNVSSYGGSTDYDSSQYNEDMKFKRMALGTQYNA 602
 Db 610 VVRALDTELEATIDTNGMRPGSQV-----FDSRQCSAQIRMEQMAFGSQDYSS 659

RESULI 15

AAB74206

ID AAB74206 standard; protein; 731 AA.

XX

AC AAB74206;

XX

DT 17-MAY-2001 (first entry)

XX

DE Protein encoded by Arabidopsis gene #1.

XX

KW Proline-rich extensin-like receptor kinase; PERK; resistance;

XX

KW plant.

XX

OS Arabidopsis thaliana.

XX

PN WO200114563-A1.

XX

PD 01-MAR-2001.

XX

PF 18-AUG-2000; 2000WO-CA009566.

XX

PR 19-AUG-1999; 99US-0149466.

XX

PR 13-OCT-1999; 99US-0159122.

XX

PA (GRI/)/ GORING D.

XX

PA (SILV/)/ SILVA N.

XX

PI Goring D, Silva N;

XX

DR WPI; 2001-244305/25.

XX

PT New proline-rich, extensin-like receptor kinase nucleic acids and

PT polypeptides useful for increasing plant wounding or pathogen
 PT resistance, or for producing transgenic plants with increased wounding
 or pathogen resistance -

XX Examples; Fig 11; 9lpp; English.

XX The present invention relates to proline-rich extensin-like
 CC receptor kinase (PERK). The PERK nucleic acids and polypeptides
 CC are useful for increasing the resistance of plants to wounding
 CC and pathogens. These are also useful for producing transgenic
 CC plants with increased wounding and pathogen resistance compared
 CC with a wild type plant, as well as in assays for identifying
 CC and developing compounds to inhibit and/or enhance polypeptide
 CC function directly.

XX Sequence 731 AA;

Query Match 41.0%; Score 1415.5; DB 22; Length 731;
 Best Local Similarity 43.4%; Pred. No. 5.4e-70;
 Matches 321; Conservative 93; Mismatches 156; Indels 169; Gaps 22;

QY 2 SSAPSPGTGSPSPSPSNTTT-----TPPPAS-----APPTTTPSPSP 40
 Db 29 NSALPPVDSPPSPPADSSSTPPLSEPTSPDPDSQLPPLPSILPLTDSPPSPSPSP 88
 QY 41 PSTIPIPSPPSRSTPSAP-----PPSPPTSTFGSPSP-----LPQSPPA-----PTTP 86
 Db 89 DST-PSPPPTTSNPSPPDESETPPAPNESNDNNPPPSQDLPSPSPSPSPNVPNT 147
 QY 87 GSP--APVTPEPTNP-----PPSPVPPSPNP-----SREGSPRPPSPSP----- 129
 Db 148 ESPPLQSPPAFPASDPTNSPASPDPDTPNPPIQPSGATSPFANPNAPSPSPFPVPPKT 207
 QY 130 -----SSDGLSTG-----VVVGIATGVALLVIVTLCIL 159
 Db 208 PSSGPFVSPSTSPSKGTFTPNQGGDGGGGGGYQGTMTVMGAVAGFALIGVFLV 267
 QY 160 CKKKRRDEEDAY-----VYVPP-----PPGPKAGGYGGQQQWROONATP 202
 Db 268 RKKKR--NIDSYNHSQYLPHNFSVKSDGLYGQDPCKGYSYGSGNNGSYNNSSQOOSM 325
 QY 203 PSDHVVTSLPPPAPSPRPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPP 262
 Db 326 GNSYGTAG-----GGYPHHQ-----MQSSGTPD-----SAILGSGQTH 358
 QY 263 FYEELARVNFSEANLGGGFGYVHKGVLPKGVEAVVVKLVKVGSGGERFOAEVEI 322
 Db 359 FSYEELAEITQGFARKNILGEGFGCVYKGTLDGKVVAVKQKAGSGQDREFKAEVEI 418
 QY 323 ISRVHHRHLSLVGYCIAGAKRLLVYEFVPPNNLELHLCGERPTMEWTRKIALGSAK 382
 Db 419 ISRVHHRHLSLVGYCISDQHRLLIEFVSQTLLEHLH-----EMSKVRVIAIGSAK 471
 QY 383 GLSLHEDCNPKIHRDIKASNILIDFKFAK-----VADEGLAKIA 424
 Db 472 GLAYLEHEDCHPKIHRDIKASNILIDDEYEAQATMKSSFSLNLSYDCKVLVADFGLARLN 531
 QY 425 SDTNTHVSTRVMTGTYLAPEYAAKGLTEKSDVTFSGVVLLELITGRPPVDANNVYD 484
 Db 532 DTTQTHVSTRVMTGTYLAPEYAAKGLTEKSDVTFSGVVLLELITGRPPVDQTPQLEE 591
 QY 485 SLVDWARPPLNRASEOGDFEGLADAKNNNGYDREEMARVACAAACVRSARRPRMSQI 544
 Db 592 SILVENARPLLLKALETGDLSELIDTRLEKRYVEHEVFRMIETAAACVRSARRPRMSQ 651
 QY 545 VRALEGNVSLDNEGMRPGQSNVSSYGGSTDYDSSQYNEDMKFKRMALGTQYNA 604
 Db 652 VRALDGDGSDISNGIKIGQ-----STTYDSQYINEDIMKFKRMAGGSDNSVESG 702
 QY 605 EYSNPTSDGLYPSGSSSE 623
 Db 703 LYS-----GNYSKSSSD 715

Tue Jul 8 08:52:59 2003

us-10-086-464-2.rag

Page 13

Search completed: July 2, 2003, 15:22:14
Job time : 76 secs

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OM protein - protein search, using sw model

Run on: July 2, 2003, 14:57:12 ; Search time 18 Seconds
(without alignments)
1057.591 Million cell updates/sec

Title: US-10-086-464-2
Perfect score: 3453
Sequence: 1 MSSAPSGTOSPPSPNSMT.....REMEMGKIKRTGGYSGPSL 647

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
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2: /cgn2_5/ptodata/1/iaa/5B.COMB.pep.*
3: /cgn2_5/ptodata/1/iaa/6A.COMB.pep.*
4: /cgn2_5/ptodata/1/iaa/6B.COMB.pep.*
5: /cgn2_5/ptodata/1/iaa/PCUS.COMB.pep.*
6: /cgn2_5/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|---------------------|-------------------|
| 1 | 754.5 | 21.9 | 968 | 4 US-09-228-986-76 | Sequence 76, Appl |
| 2 | 736 | 21.3 | 630 | 4 US-09-228-986-71 | Sequence 71, Appl |
| 3 | 703.5 | 20.4 | 707 | 4 US-09-228-986-80 | Sequence 80, Appl |
| 4 | 678 | 19.6 | 638 | 4 US-09-228-986-74 | Sequence 74, Appl |
| 5 | 604.5 | 17.5 | 1196 | 4 US-08-881-706-2 | Sequence 2, Appl |
| 6 | 593 | 17.2 | 903 | 4 US-09-228-986-78 | Sequence 78, Appl |
| 7 | 579.5 | 16.8 | 980 | 2 US-08-473-553A-6 | Sequence 6, Appl |
| 8 | 575 | 16.7 | 858 | 2 US-08-265-628-2 | Sequence 2, Appl |
| 9 | 572.5 | 16.6 | 985 | 1 US-07-717-331F-2 | Sequence 2, Appl |
| 10 | 572 | 16.6 | 857 | 1 US-07-717-331F-2 | Sequence 2, Appl |
| 11 | 566.5 | 16.4 | 666 | 4 US-09-228-986-68 | Sequence 68, Appl |
| 12 | 560.5 | 16.2 | 632 | 4 US-09-228-986-77 | Sequence 77, Appl |
| 13 | 552 | 16.0 | 282 | 2 US-08-473-553A-7 | Sequence 4, Appl |
| 14 | 545 | 15.8 | 321 | 1 US-08-447-185-1 | Sequence 1, Appl |
| 15 | 545 | 15.8 | 544 | 2 US-08-587-680A-25 | Sequence 25, Appl |
| 16 | 543 | 15.7 | 655 | 4 US-09-228-986-70 | Sequence 70, Appl |
| 17 | 539.5 | 15.6 | 857 | 1 US-07-717-331F-3 | Sequence 3, Appl |
| 18 | 525 | 15.2 | 999 | 2 US-08-473-553A-5 | Sequence 5, Appl |
| 19 | 506 | 14.7 | 712 | 1 US-08-587-889-2 | Sequence 2, Appl |
| 20 | 506 | 14.7 | 712 | 2 US-08-980-060-5 | Sequence 5, Appl |
| 21 | 506 | 14.7 | 712 | 4 US-09-307-185-5 | Sequence 5, Appl |
| 22 | 506 | 14.7 | 712 | 5 PCI-US96-09193-2 | Sequence 2, Appl |
| 23 | 495 | 14.3 | 659 | 4 US-09-228-986-75 | Sequence 75, Appl |
| 24 | 486 | 14.1 | 739 | 4 US-09-503-922-1 | Sequence 1, Appl |
| 25 | 456.5 | 13.2 | 711 | 4 US-09-228-986-79 | Sequence 79, Appl |
| 26 | 430 | 12.5 | 690 | 4 US-09-228-986-69 | Sequence 69, Appl |
| 27 | 393.5 | 11.4 | 1025 | 2 US-08-567-375-4 | Sequence 4, Appl |

| | | | | | |
|----|-------|------|------|---------------------|-------------------|
| 28 | 393.5 | 11.4 | 1025 | 2 US-08-587-680A-4 | Sequence 4, Appl |
| 29 | 368 | 10.7 | 1012 | 2 US-08-475-891A-4 | Sequence 4, Appl |
| 30 | 367.5 | 10.6 | 501 | 2 US-08-980-060-6 | Sequence 6, Appl |
| 31 | 367.5 | 10.6 | 501 | 4 US-09-307-185-6 | Sequence 6, Appl |
| 32 | 367.5 | 10.6 | 947 | 4 US-09-228-986-73 | Sequence 73, Appl |
| 33 | 351 | 10.2 | 1023 | 2 US-08-475-891A-2 | Sequence 2, Appl |
| 34 | 351 | 10.2 | 1023 | 2 US-08-567-375-2 | Sequence 2, Appl |
| 35 | 351 | 10.2 | 1023 | 2 US-08-587-680A-2 | Sequence 2, Appl |
| 36 | 347 | 10.0 | 913 | 1 US-08-445-640-4 | Sequence 4, Appl |
| 37 | 347 | 10.0 | 913 | 3 US-08-170-558-4 | Sequence 4, Appl |
| 38 | 347 | 10.0 | 913 | 3 US-08-447-314-4 | Sequence 4, Appl |
| 39 | 347 | 10.0 | 913 | 3 US-08-445-461-4 | Sequence 4, Appl |
| 40 | 341 | 9.9 | 919 | 1 US-08-336-343A-2 | Sequence 2, Appl |
| 41 | 331.5 | 9.6 | 330 | 1 US-08-642-255-32 | Sequence 32, Appl |
| 42 | 331.5 | 9.6 | 408 | 1 US-07-609-716-65 | Sequence 65, Appl |
| 43 | 331.5 | 9.6 | 408 | 4 US-08-475-411A-65 | Sequence 65, Appl |
| 44 | 331.5 | 9.6 | 408 | 4 US-08-478-029A-65 | Sequence 65, Appl |
| 45 | 329.5 | 9.5 | 297 | 2 US-08-580-545B-6 | Sequence 6, Appl |

ALIGNMENTS

RESULT 1
US-09-228-986-76
; Sequence 76, Application US/09228986
; Patent No. 6359198
; GENERAL INFORMATION:
; APPLICANT: Strabala, Timothy
; TITLE OF INVENTION: Compositions Isolated from Plant Cells
; TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signalling
; FILE REFERENCE: 11000/1020
; CURRENT APPLICATION NUMBER: US/09/228, 986
; CURRENT FILING DATE: 1999-01-12
; NUMBER OF SEQ ID NOS: 130
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 76
; LENGTH: 968
; TYPE: PRT
; ORGANISM: Eucalyptus grandis
US-09-228-986-76

Query Match 21.9%; Score 754.5; DB 4; Length 968;
Best Local Similarity 35.3%; Pred. No. 1.2e-35;
Matches 184; Conservative 89; Mismatches 133; Indels 115; Gaps 16;

| | | | |
|----|-----|--|-----|
| QY | 118 | PRPSSP-----SP---PSPSSDGLSTGVVIGVIGVALLVIVILCLCKKKRRDEE | 169 |
| DB | 533 | PKRPFPGYYFTASPYAFPDNGGTALSKGVIVIGVIGVALLVIVILCLCKKKRAEK | 592 |
| QY | 170 | DAYVYPP-----PPPGKAGPYGGQOQOQONATPPSDHVTSLPPPKAPSPRPP | 225 |
| DB | 593 | -----ALESRPFASWAPSGKDSGAPOLKGRW----- | 621 |
| QY | 226 | PPPPPPMSSSGGSDYSDRVPVLPPLPPSGLVLFSGKSTFTYEELARATNGFSEANLGGG | 285 |
| DB | 622 | -----FSYDELKRCITNFSNDSNELGFGG | 644 |
| QY | 286 | FGYVHKGLPFGKEVAVKOLKVGSGOGERFQAEVILSRVHHRLVSLVGYCYAGAKRL | 345 |
| DB | 645 | YGVYRGLVDPGHILAIKRAQCSMQGATEFKTEILLSRVHHKNDVLGLGFCFCEQGEQM | 704 |
| QY | 346 | LVYEFVNNLHLHGHGCRPTMEWSTRLKIALGSAKGLSVLHDCNPKIHRDIKASNI | 405 |
| DB | 705 | LVYEFVNNLHLHGHGCRPTMEWSTRLKIALGSAKGLSVLHDCNPKIHRDIKASNI | 764 |
| QY | 406 | LIDFKEAKVADFGGLAKIASDTNT--HVSTWMTGTFGLAPEYASGKLTSEKSDVFSGVV | 464 |
| DB | 765 | LLDEHLTAKVADFGGLAKIASDTNT--HVSTWMTGTFGLAPEYASGKLTSEKSDVFSGVV | 824 |
| QY | 465 | LLLELTGRRPVDANNVYDDSLVDWAPPLNRRASEQDFFG---LADAKNN--GYDREEM | 520 |

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Db      825 MLEELZTAQKQIEKGVVRE-----INTAMKNDQ--DIYGVREMDPMSRSMGY-LVGF 876
QY      521 ARWACAAACVRESARRRRPMQVIALFENYSLDNEGRMGQSNVTSYSGGSDYDXS 580
Db      877 SRFLDIAMRCVBSAARDRTMSEVKAIEIQLQ-----NDGIHNTSASSS---AIDFGS 929
QY      581 SQ-----YNEDMKFRKALGTQENATGEYSNPTSIDGL 615
Db      930 TKGAPRHPINDALPK-----KEVSYSDSFDYS---GGYGL 961

RESULT 2
US-09-228-986-71
; Sequence 71, Application US/09228986
; Patent No. 6359198
; GENERAL INFORMATION:
; APPLICANT: Strabala, Timothy
; APPLICANT: Nieuwenhuizen, Niels
; TITLE OF INVENTION: Compositions Isolated from Plant Cells
; FILE REFERENCE: 11000/1020
; CURRENT APPLICATION NUMBER: US/09/228,986
; CURRENT FILING DATE: 1999-01-12
; NUMBER OF SEQ ID NOS: 130
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 71
; LENGTH: 630
; TYPE: PRT
; ORGANISM: Pinus radiata
US-09-228-986-71

Query Match      21.3%; Score 736; DB 4; Length 630;
Best Local Similarity 37.2%; Pred. No. 8.6e-35;
Matches 175; Conservative 68; Mismatches 125; Indels 102; Gaps 12;

QY      90 PAPVPTPTNPPSPVPPPP-----SNPSREGGPRPPSPSPSPSDGLSTGVVYGIATGG 146
Db      208 PCGSPSPSPPPPPPPPPVAGSNGARVQSSS-----STGAIAGGYAAG 251
QY      147 VALLVIVTLCCLCKKRRDEEDAYVPPPPPGPKAGPYGGQQQWROQNATPPPSDH 206
Db      252 AALLF-----AAPAIGFAW-----WRRRK---PQEH 274
QY      207 VVTSLSPPPKAPSPRPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPP 266
Db      275 -----FEDVPA---EEDPEVHLGQLK-RFSIR 297
QY      267 ELARATNGFSANLLGGGGYVHKVLPSCGEVAVKOLK-VGSGGGEREFOAEVEILSR 325
Db      298 ELQVATDGFNRNLTGRRGGKVKYKGLADGSLVAVKRIKEERTPGGELQFOTEVEMISM 357
QY      326 VHRRLVSLVGYCTAGAKRLIVYEFVNNLE--LHLHGEPRPMWSTRLKIALGSAKG 383
Db      358 AVHNLRLRGFCMTPTERLLVVPYMWANGSVASCLRERACQNDPLDWPTKRRIALGSARG 417
QY      384 LSYLHEDCNPKIIHROIKASNILIDFKFAKVADEFLAKLASDNTHTVSTRVMTGFLA 443
Db      418 LSYLHEDCDPKIIHROVKAANILLDEYEAUVGDFGLAKMDYKDTHTVAVRTGTGIIA 477
QY      444 PEYASGKLTESDVSFVGWLELTIGTRRPVANNVYDVS--LVDWAPRLINRASEQG 501
Db      478 PEYLSGKSEKTDVFGYGMLELTIGQAFDLARLANDDDVYMLLDWVKGLL---KER 533
QY      502 DFEGLADAKNNYDREEMARVACAAACVYHARRRPMRSQIVRALEGN 551
Db      534 RLDMLVDPLDKNVYEAEBQLIQVALLCTQGSMPDRPKMSEVVRMLEGD 583

RESULT 3
US-09-228-986-80
; Sequence 80, Application US/09228986
; Patent No. 6359198
; GENERAL INFORMATION:
; APPLICANT: Strabala, Timothy
; APPLICANT: Nieuwenhuizen, Niels
; TITLE OF INVENTION: Compositions Isolated from Plant Cells
; FILE REFERENCE: 11000/1020
; CURRENT APPLICATION NUMBER: US/09/228,986
; CURRENT FILING DATE: 1999-01-12
; NUMBER OF SEQ ID NOS: 130
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 74
; LENGTH: 638
; TYPE: PRT

```

```

; APPLICANT: Strabala, Timothy
; APPLICANT: Nieuwenhuizen, Niels
; TITLE OF INVENTION: Compositions Isolated from Plant Cells
; TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signalling
; FILE REFERENCE: 11000/1020
; CURRENT APPLICATION NUMBER: US/09/228,986
; CURRENT FILING DATE: 1999-01-12
; NUMBER OF SEQ ID NOS: 130
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 80
; LENGTH: 707
; TYPE: PRT
; ORGANISM: Pinus radiata
US-09-228-986-80

Query Match      20.4%; Score 703.5; DB 4; Length 707;
Best Local Similarity 34.0%; Pred. No. 6.8e-33;
Matches 178; Conservative 81; Mismatches 179; Indels 85; Gaps 14;

QY      84 TTPGSPAPVPTPTNPPSPVPPSPNPSREGGSPRPPSPSPSPSDG-----L 134
Db      247 TGPAPPPPTTP-----PPSN-----NRPPKSSNVVPSGGSGKGNKSL 289
QY      135 STGVVVGIAIGVALLVIVTLCCLCKKRRDEEDAYVPPPPPGPKAGPYGGQQQ 194
Db      290 SGAIVGIIIFAVILLTVAAAILGVILYARKSPREED-----EKL 329
QY      195 WROQNATP--PSDHVVTSLPPPKAPSPRPPPPPPPPPPPPPPPPPPPPPPPP 247
Db      330 SNRVSTPLSLDPAELIKESPEQKVSSSPLEIALKPPSPERNKSTGDKGFSIFSKRTK 389
QY      248 PPPSPGLVGFSGKSTFTYEELARATNGEFAENLLGGGGYVHKVLPSCGEVAVKOLK 307
Db      390 NP-----ISATEYSTADLQMA:NSFQDNLIAEGALGRYRAEFPGKILAVKLD 441
QY      308 G--SGGGEREFOAEVEILSRVHRHLVSLVGYCTAGAKRLIVYEFVNNLE--ELH 363
Db      442 STLSLQRPEDFLDAYSINISRLHPKTELGYCTEHEQVLLVYFDNGLSDVLMHDE 501
QY      364 GRPTWENSTRUKIALGSAKGLSYLHEDCNPKIIHROIKASNILIDFKFAKVADEFLAK 423
Db      502 TTRNLNIRKIALGSAKGLSYLHEDCNPKIIHROIKASNILIDFKFAKVADEFLAK 423
QY      424 ASDTNHIVSTRVMTGFLAPEYASGKLTESDVSFVGWLELTIGTRRPVANNVYD 483
Db      560 ALNPNSERQVQLGSEFSAPEYVMSGIYTMKSDVIFGVVMELELTIGTRRPVANNVYD 619
QY      484 DSLVDWAPRLINRASEQGFESLA--DAKNNGYDREEMARVACAAACVYHARRRPR 540
Db      620 QSLVRWATPOLH-----DIDALAKKVDPAKGSYPAKSLSRFADILALCIQPEFE 573
QY      541 MSQIVRALEGNVSLDANEGMRPGOSNYVSYSGGSDYDSSOY 583
Db      674 MSEVVQALVRMQRASLNKRTMGDE-----TADHDPADY 707

RESULT 4
US-09-228-986-74
; Sequence 74, Application US/09228986
; Patent No. 6359198
; GENERAL INFORMATION:
; APPLICANT: Strabala, Timothy
; APPLICANT: Nieuwenhuizen, Niels
; TITLE OF INVENTION: Compositions Isolated from Plant Cells
; FILE REFERENCE: 11000/1020
; CURRENT APPLICATION NUMBER: US/09/228,986
; CURRENT FILING DATE: 1999-01-12
; NUMBER OF SEQ ID NOS: 130
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 74
; LENGTH: 638
; TYPE: PRT

```



```

1  TITLE OF INVENTION:  Transformed Plants, and Proteins
2
3  NUMBER OF SEQUENCES:  11
4
5  CORRESPONDENCE ADDRESS:
6
7  ADDRESSEE:  Flehr, Hohnbach, Test, Albritton & Herbert
8
9  STREET:  Four Embarcadero Center, Suite 3400
10
11  CITY:  San Francisco
12
13  STATE:  California
14
15  COUNTRY:  United States
16
17  ZIP:  94111-4187
18
19  COMPUTER READABLE FORM:
20
21  MEDIUM TYPE:  Floppy disk
22
23  COMPUTER:  IBM PC compatible
24
25  OPERATING SYSTEM:  PC-DOS/MS-DOS
26
27  SOFTWARE:  PatentIn Release #1.0, Version #1.30
28
29  CURRENT APPLICATION DATA:
30
31  APPLICATION NUMBER:  US/08/473,553A
32
33  FILING DATE:  08-JUN-1995
34
35  CLASSIFICATION:  800
36
37  ATTORNEY/AGENT INFORMATION:
38
39  NAME:  Silva, Robin M.
40
41  REGISTRATION NUMBER:  38,304
42
43  REFERENCE/DOCKET NUMBER:  A-60886/RFT/RMS
44
45  TELECOMMUNICATION INFORMATION:
46
47  TELEPHONE:  (415) 781-1989
48
49  TELEFAX:  (415) 398-3249
50
51  TELEX:  910 277299
52
53  INFORMATION FOR SEQ ID NO:  6:
54
55  SEQUENCE CHARACTERISTICS:
56
57  LENGTH:  980 amino acids
58
59  TYPE:  amino acid
60
61  STRANDEDNESS:  unknown
62
63  TOPOLOGY:  unknown
64
65  MOLECULE TYPE:  protein
66
67  US-08-473-553A-6

```

Query Match 16.8%; Score 579.5; DB 2; Length 980;
Best Local Similarity 34.8%; Pred. NO. 1.1e-25;
Matches 139; Conservative 65; Mismatches 134; Indels 61

[illegible]

RESULT 8

US-08-265-638-2
; Sequence 2, Application US/08265628
; Patent No. 5821094
; GENERAL INFORMATION:

APPLICANT: Rothstein, Steven J.
 APPLICANT: Goring, Daphne
 TITLE OF INVENTION: S-LOCUS RECEPTOR KINASE GENE IN A
 TITLE OF INVENTION: SELF-INCOMPATIBLE BRASSICA NAPUS LINE
 NUMBER OF SEQUENCES: 10
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: McAndrews, Held & Malloy, Ltd.
 STREET: 500 W. Madison St. Suite 3400
 CITY: Chicago
 STATE: Illinois
 COUNTRY: USA
 ZIP: 60661
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/265,628
 FILING DATE:
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/07/959,945
 FILING DATE:
 APPLICATION NUMBER: US 07/247,564
 FILING DATE: 03-MAR-1992
 ATTORNEY/AGENT INFORMATION:
 NAME: Pochopien Ph.D., Donald J.
 REGISTRATION NUMBER: 32,167
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 312-707-8889
 TELEFAX: 312-707-9155
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 858 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-265-628-2

Query Match 16.7%; Score 575; DB 2; Length 858;
Best Local Similarity 39.6%; Pred. No. 1.7e-25;
Matches 130; Conservative 65; Mismatches 120; Indels

| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
|-----|----|----|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|-----|-----|---|-----|---|---|-----|---|---|---|--|-----|
| 266 | QY | BE | L | A | R | A | T | N | G | F | E | A | N | L | G | G | F | Y | V | H | K | G | V | L | P | S | G | E | V | A | K | E | K | Y | S | S | G | G | E | R | F | O | A | E | V | I | I | S | R | | 325 | | | | | | | | |
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| 520 | Db | E | A | V | K | A | T | E | N | F | N | C | N | K | I | G | G | F | I | V | Y | K | R | L | D | Q | E | I | A | V | K | R | L | S | K | T | S | V | Q | G | T | E | F | N | V | R | L | A | R | | 579 | | | | | | | | |
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| 326 | QY | V | H | R | H | L | S | Y | G | T | A | K | R | L | I | V | E | F | V | P | N | N | L | H | J | H | E | G | R | - | P | T | N | E | S | T | R | L | K | I | A | L | S | A | K | L | | 384 | | | | | | | | | | | |
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| 580 | Db | L | O | H | I | N | L | V | R | I | L | G | C | E | A | D | E | K | M | - | V | Y | E | L | N | L | S | D | S | Y | L | F | G | N | K | R | S | I | L | N | K | O | R | F | N | I | T | G | V | A | R | L | | 639 | | | | | |
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| 385 | QY | S | Y | L | H | E | D | C | N | P | K | I | T | H | R | D | I | K | A | S | N | I | L | D | E | F | A | K | V | A | D | G | L | A | K | I | A | S | D | T | N | T | H | V | S | T | R | - | V | M | G | T | F | G | Y | L | A | | 443 |
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| 640 | Db | L | I | C | H | Q | S | R | F | I | L | H | D | K | M | V | S | N | I | L | D | K | N | T | M | P | K | I | S | D | F | G | M | A | R | I | F | A | R | D | E | A | N | T | R | K | V | G | T | G | Y | S | | 699 | | | | | |
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| 444 | QY | P | E | X | A | S | K | L | E | K | S | D | V | F | G | V | L | L | E | I | T | G | R | P | D | A | N | N | V | T | D | S | L | V | D | - | W | A | R | P | L | N | A | R | S | O | G | | 501 | | | | | | | | | | |
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| 700 | Db | P | E | A | M | D | G | V | F | E | K | S | D | V | F | E | G | V | I | V | E | I | V | S | G | R | K | R | G | F | T | N | L | H | E | N | N | L | S | Y | V | W | S | H | T | E | G | R | A | L | I | V | | 759 | | | | | |
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| 502 | QY | D | - | - | - | F | E | G | L | A | D | K | N | N | G | Y | D | R | E | A | M | V | A | C | A | A | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT 9

US-08-473-553A-2
; Sequence 2, Application US/08473553A
; Patent No. 5859338

GENERAL INFORMATION:
APPLICANT: Meyerowitz, Elliot M.
APPLICANT: Clark, Steven E.
APPLICANT: Williams, Robert W.
TITLE OF INVENTION: Plant Clavatal Nucleic Acids,
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert
STREET: Four Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: California
COUNTRY: United States
ZIP: 94111-4187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/473,553A
FILING DATE: 06-JUN-1995
CLASSIFICATION: 80C
ATTORNEY/AGENT INFORMATION:
NAME: Silva, Robin M.
REGISTRATION NUMBER: 38,304
REFERENCE/DOCKET NUMBER: A-60886/RFT/RMS
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
TELEFAX: (415) 398-3249
TELEX: 910 277293
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 985 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-473-553A-2

Query Match 16.6%; Score 572.5; DB 2; Length 985;
Best Local Similarity 34.6%; Pred. No. 2.7e-25;
Matches 138; Conservative 65; Mismatches 135; Indels 61; Gaps 11;

QY 187 PYGQQQQQWQQNATPSSDHVVTSLPPPKAPSPRPPPPPPPPFSSSGSGSDYSDRPV 246
DB 598 PLGG--QFLVNETSAGNTYLCPLHRVSCPTHPGQT-----SDNNHTAL 640

QY 247 LPPPS-----PGVL-----GFSKSTFTYEELARATNGF 275
DB 641 FSPSRIVTVIAATGLILISVAITROMKKNQKSLAKLTAFQKLFKSDVLEC---L 697

QY 276 SEANLGGQGGVYHKGVLPSGKEVAYQLKVGSGGGERE--FOAEVEIISRVHRLDVS 333
DB 698 KEENIIGKGGSGVIRGSMFNNVDVAKRL-VGRGTGRSDHGFATQTLGRIRHRIVR 756

QY 334 LVGYCIAGAKRLLYEVPVNNLEHLHGEGRPTMEWSTRLKIALGSAKGLSYLHDCNP 393
DB 757 LLGVVANKONTLLIYETPMNGSLGELLHGSKGGLQWETHRVAEAAKGLCYLHDCSP 816

QY 394 KIHRDIKASNILIDFEAKVADFGLAKIASO--TNTFHVSRVMTGTYGLAPEYAASGL 452
DB 817 LILHRDVKSNILLDSFEARVADFGLAKIVDGAASECKSSIADSYGYIAPAYATLKV 876

QY 453 TEKSDVPSFGVLELITGRPPVDANNVYDDSLVDWARP-----LNRASEQDGEGLADA 509
DB 877 DEKSDVYSFGVLELITGRPPVDANNVYDDSLVDWARP-----LNRASEQDGEGLADA 509

QY 510 KMNNGYDREEMARVACAAACVHRSARRRRPMSQIVRAL 548
DB 935 RL-TGYPLTSLVHVKIAMCVEEAAARPTMREVVHML 972

RESULT 10

US-07-717-331F-2
Sequence 2, Application US/07717331F
Patent No. 5484905
GENERAL INFORMATION:
APPLICANT: June Nasrallah; Michael Nasrallah; and Joshua
APPLICANT: Stein
TITLE OF INVENTION: A Receptor Protein Kinase Gene
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Yahwak & Associates
STREET: 25 Skytop Drive
CITY: Trumbull
STATE: Connecticut
COUNTRY: USA
ZIP: 06611
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
COMPUTER: Macintosh
OPERATING SYSTEM: MS-DOS
SOFTWARE: Microsoft Word
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/717,331F
FILING DATE: June 19th 1991
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: George M. Yahwak
REGISTRATION NUMBER: 26,824
TELECOMMUNICATION INFORMATION:
TELEPHONE: (203)268-1951
TELEFAX: (203)268-1951
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 857 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-07-717-331F-2

Query Match 16.6%; Score 572; DB 1; Length 857;
Best Local Similarity 32.3%; Pred. No. 2.5e-25;
Matches 139; Conservative 83; Mismatches 119; Indels 90; Gaps 11;

QY 135 STGVVVGIAIGVALLIVTLICLCCKRRDEEDAYVPPPPPPGKAGGPGGQQQ 194
DB 443 ASGKIISLTV-GSVLLLLIMFC-LWKRKQKRAKASISIAN----- 482

QY 195 WROQNATPSSDHVVTSLPPPKAPSPRPPPPPPPPFSSSGSDYSDRPVLPSPGL 254
DB 483 -TQNNQPLFMEMVLS----- 497

QY 255 VLGFSSKSTFT-----YEEL-----ARATNGFSEANLLGGQGGVYHKGVLPSGKEV 300
DB 498 ---SKREFSGEYKEELELEPLIEMETVVKATENESSCKNLGGQGGVYHKGVLPSGKEV 553

QY 301 AVKQLKVGSGGGEREFOAEVEIISRVHRLVSLGYCIAGAKRLLYEVEFVNNLEHL 360
DB 554 AVKRLSKTSVQGTDEFMNEVTILARQLHNLVQLGCCIEGDEKMLIYELENLSLSYL 613

QY 361 HGEGRPT-MEWSTRLKIALGSAKGLSYLHDCNPKIHRDIKASNILIDFEAKVADFG 419
DB 614 FGKTRRSKLNLRNEDITNGVARGLLYLHQDSRFRIHRDLKVSNILDKNNMIPKISDFG 673

QY 420 LAKIASOTNTHVST-RVMGTGTYGLAPEYAASGLTEKSDVFSFGVLELITGRPPVDAN 478
DB 674 MARFERDETANTMKVGVYGYMSPEYAMGIFSEKSDVFSFGVLEIYVSGKKNRGEY 733

QY 479 NVYVDDSLVD--WAPRLNRASEQDGEGLADAKMNG--YDREEMARVACAAACVHRS 534
DB 734 NLDYENDLLSVWSNWKSGRALEIVD-PVIVDSLSQPSITQPQEVLCIQIGLLCVQEL 792

QY 535 ARRRPMSQIV 545

Query Match 15.8%; Score 545; DB 1; Length 321;
Best Local Similarity 38.0%; Pred. No. 3.2e-24;
Matches 123; Conservative 57; Mismatches 132; Indels 12; Gaps 5;

| | | | | | | |
|-----|----|-----|---------|--------------------|--|-----|
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| 2 | QY | GS | SKATNS | INDALS | SSYLVPFESYRPLVDLEAATNDFHKLFGHGVGVKGVLR | 61 |
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| 414 | QY | KV | ADFLG | LAKIASDPTN--THVSTR | VYMGTVGYLAPVAASGKLTEKSDYFSGVWLELITCR | 472 |
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| 473 | QY | RP | VANNVY | DDSLDWARPLLNRAS | QSGDFGLADKANNNGYDREMARVACAAACVR | 532 |
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RESULT 15
US-08-587-680A-25
Sequence 25, Application US/08537680A
Patent No. 5977434
GENERAL INFORMATION:
APPLICANT: Ronald, Pamela C.
APPLICANT: Wang, Guo-Liang
APPLICANT: Song, Wen-Yuang
APPLICANT: Szabo, Veronique
TITLE OF INVENTION: Procedures and Materials for Conferring
TITLE OF INVENTION: Disease Resistance in Plants
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.3C
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/587,680A
FILING DATE: 17-JAN-1996
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,375

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/ FILING DATE: 17-JAN-1995
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/475,891
/ FILING DATE: 07-JUN-1995
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 60/004,645
/ FILING DATE: 29-SEP-1995
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/567,375
/ FILING DATE: 04-DEC-1995
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Bastian, Kevin L.
/ REGISTRATION NUMBER: 34,774
/ REFERENCE/DOCKET NUMBER: 023070-0589400S
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (415) 576-0200
/ TELEFAX: (415) 576-0300
/ INFORMATION FOR SEQ ID NO: 25:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 544 amino acids
/ TYPE: amino acid
/ STRANDEDNESS:
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ FEATURE:
/ NAME/KEY: Protein
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US-08-587-680A-25

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Matches 125; Conservative 59; Mismatches 111; Indels 12; Gaps 7;

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Db | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 542 SQIVRAL 548
Db | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 526 REVVQML 532
Db | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
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Search completed: July 2, 2003, 15:16:13
Job time : 21 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: July 2, 2003, 15:13:41 ; Search time 35 Seconds
(without alignments)
2125.726 Million cell updates/sec

Title: US-10-086-464-2

Perfect score: 3453

Sequence: 1 MSSAPSPGPGSPSPSPSPNST.....REMEMGKIKRTGGYSGPSL 647

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 440963 seqs, 114992915 residues

Total number of hits satisfying chosen parameters: 440863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications_AA:*

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- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
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- 14: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | % Match | Query Length | ID | Description |
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| 1 | 3453 | 100.0 | 647 | US-10-086-464-2 | Sequence 2, Appli |
| 2 | 3453 | 100.0 | 647 | US-10-086-464-4 | Sequence 4, Appli |
| 3 | 3453 | 100.0 | 721 | US-10-086-464-5 | Sequence 5, Appli |
| 4 | 1748.5 | 50.6 | 633 | US-10-086-464-11 | Sequence 11, Appli |
| 5 | 1587 | 48.9 | 674 | US-10-086-464-14 | Sequence 8, Appli |
| 6 | 1415.5 | 41.0 | 731 | US-10-086-464-8 | Sequence 17, Appli |
| 7 | 1399 | 40.5 | 731 | US-10-086-464-17 | Sequence 71, Appli |
| 8 | 754.5 | 21.9 | 968 | US-10-101-464A-75 | Sequence 27, Appli |
| 9 | 736 | 21.3 | 630 | US-10-101-464A-71 | Sequence 927, App |
| 10 | 722 | 20.9 | 629 | US-09-828-313-27 | Sequence 927, App |
| 11 | 704.5 | 20.4 | 749 | US-10-101-464A-80 | Sequence 80, Appli |
| 12 | 703.5 | 20.4 | 707 | US-10-101-464A-82 | Sequence 74, Appli |
| 13 | 678 | 19.6 | 638 | US-10-101-464A-74 | Sequence 812, App |
| 14 | 672 | 19.5 | 623 | US-10-101-464A-812 | Sequence 263, App |
| 15 | 661 | 19.1 | 366 | US-10-219-220-263 | Sequence 936, App |
| 16 | 660.5 | 19.1 | 515 | US-10-101-464A-936 | Sequence 911, App |
| 17 | 647 | 18.7 | 842 | US-10-101-464A-911 | Sequence 1099, Ap |
| 18 | 641.5 | 18.6 | 894 | US-09-754-853A-1099 | Sequence 1116, Ap |
| 19 | 641.5 | 18.6 | 894 | US-09-754-853A-1116 | |

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| 20 | 641.5 | 18.6 | 894 | 9 | US-09-754-853A-1117 | Sequence 1117, Ap |
| 21 | 641.5 | 18.6 | 894 | 9 | US-09-754-853A-1118 | Sequence 1118, Ap |
| 22 | 641.5 | 18.6 | 894 | 9 | US-09-754-853A-1119 | Sequence 1119, Ap |
| 23 | 641 | 18.6 | 744 | 9 | US-10-101-464A-942 | Sequence 942, App |
| 24 | 636.5 | 18.4 | 524 | 9 | US-10-101-464A-943 | Sequence 943, App |
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| 26 | 626.5 | 18.1 | 365 | 9 | US-10-101-464A-510 | Sequence 510, App |
| 27 | 624 | 18.1 | 919 | 9 | US-10-101-464A-642 | Sequence 642, App |
| 28 | 624 | 18.1 | 1133 | 9 | US-10-101-464A-809 | Sequence 809, App |
| 29 | 613 | 17.9 | 794 | 9 | US-10-149-846-2 | Sequence 2, Appli |
| 30 | 612.5 | 17.7 | 502 | 9 | US-10-101-464A-945 | Sequence 945, App |
| 31 | 605 | 17.5 | 901 | 9 | US-10-208-948-16 | Sequence 16, Appli |
| 32 | 604.5 | 17.5 | 1021 | 9 | US-10-101-464A-954 | Sequence 954, App |
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| 35 | 601 | 17.4 | 827 | 9 | US-10-101-464A-915 | Sequence 915, App |
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| 37 | 587.5 | 17.0 | 974 | 9 | US-10-101-464A-921 | Sequence 921, App |
| 38 | 580.5 | 16.8 | 1014 | 9 | US-10-101-464A-807 | Sequence 807, App |
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| 41 | 566.5 | 16.4 | 666 | 9 | US-10-101-464A-68 | Sequence 68, Appli |
| 42 | 565 | 16.4 | 960 | 8 | US-08-910-386A-18 | Sequence 18, Appli |
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| 45 | 558 | 16.2 | 286 | 10 | US-09-838-955-7 | Sequence 7, Appli |

ALIGNMENTS

RESULT 1
US-10-086-464-2
; Sequence 2, Application US/10086464
; Publication No. US20020199218A1
; GENERAL INFORMATION:
; APPLICANT: GORING, Daphne R. et al.
; TITLE OF INVENTION: PROLINE-RICH EXTENSIN-LIKE RECEPTOR KINASES
; FILE REFERENCE: P 25,762-A USA
; CURRENT APPLICATION NUMBER: US/10/086,464
; CURRENT FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 10/069,304
; PRIOR FILING DATE: 2002-02-19
; PRIOR APPLICATION NUMBER: PCT/CA00/00966
; PRIOR FILING DATE: 2000-08-18
; PRIOR APPLICATION NUMBER: US 60/149,466
; PRIOR FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: US 60/159,122
; PRIOR FILING DATE: 1999-10-13
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn ver. 2.1
; SEQ ID NO 2
; LENGTH: 647
; TYPE: PRT
; ORGANISM: Brassica napus
US-10-086-464-2

Query Match 100.0%; Score 3453; DB 9; Length 647;
Best Local Similarity 100.0%; Pred. No. 9,1e-143;
Matches 647; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 2

US-10-086-464-4
; Sequence 4, Application US/10086464
; Publication No. US20020199218A1
; GENERAL INFORMATION:
; APPLICANT: GORING, Daphne R. et al.
; TITLE OF INVENTION: PROLINE-RICH EXTENSIN-LIKE RECEPTOR KINASES
; FILE REFERENCE: P 25,762-A USA
; CURRENT APPLICATION NUMBER: US/10/086,464
; CURRENT FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 10/069,304
; PRIOR FILING DATE: 2002-02-19
; PRIOR APPLICATION NUMBER: PCT/CA00/00966
; PRIOR FILING DATE: 2000-08-18
; PRIOR APPLICATION NUMBER: US 60/149,466
; PRIOR FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: US 60/159,122
; PRIOR FILING DATE: 1999-10-13
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 647
; TYPE: PRT
; ORGANISM: Brassica napus
US-10-086-464-4

Query Match 100.0%; Score 3453; DB 9; Length 647;
Best Local Similarity 100.0%; Pred. No. 9,1e-143; Indels 0; Gaps 0;
Matches 647; Conservative 0; Mismatches 0;

QY 1 MSSAPSGTGGSPSPSNSTTTTTPPASAPPTTSPSPSPSTIPTSPSSSRSTPSAPP 60
DB 1 MSSAPSGTGGSPSPSNSTTTTTPPASAPPTTSPSPSPSTIPTSPSSSRSTPSAPP 60
QY 61 PSPTPTSPGSPPLPQSPAPPTTSPSPAPVTPTRNPPSPVPGPSNPSREGSPRP 120
DB 61 PSPTPTSPGSPPLPQSPAPPTTSPSPAPVTPTRNPPSPVPGPSNPSREGSPRP 120
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RESULT 3

US-10-086-464-5
; Sequence 5, Application US/10086464
; Publication No. US20020199218A1
; GENERAL INFORMATION:
; APPLICANT: GORING, Daphne R. et al.
; TITLE OF INVENTION: PROLINE-RICH EXTENSIN-LIKE RECEPTOR KINASES
; FILE REFERENCE: P 25,762-A USA
; CURRENT APPLICATION NUMBER: US/10/086,464
; CURRENT FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 10/069,304
; PRIOR FILING DATE: 2002-02-19
; PRIOR APPLICATION NUMBER: PCT/CA00/00966
; PRIOR FILING DATE: 2000-08-18
; PRIOR APPLICATION NUMBER: US 60/149,466
; PRIOR FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: US 60/159,122
; PRIOR FILING DATE: 1999-10-13
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 721
; TYPE: PRT
; ORGANISM: Brassica napus
US-10-086-464-5

Query Match 100.0%; Score 3453; DB 9; Length 721;
Best Local Similarity 100.0%; Pred. No. 1e-142; Indels 0; Gaps 0;
Matches 647; Conservative 0; Mismatches 0;

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361 HGEGRPTMEWSTRLKIALGSAKLSYLHEDCNPKIIHROIKASNILDFXFAKVADEGL 420
391 HGEGRPTMEWSTRLKIALGSAKLSYLHEDCNPKIIHROIKASNILDFXFAKVADEGL 450
421 AKTASDNTHTVSTVMGTFCGLAPEYAAAGKLTGKSDVFSFGVVLLELITGRPPVDANNV 480
451 AKTASDNTHTVSTVMGTFCGLAPEYAAAGKLTGKSDVFSFGVVLLELITGRPPVDANNV 510
481 YVDDSLVDMARPLINRASEQDCEGLADAKMNNGYDREEMARVACAAACVRRHSARRPR 540
511 YVDDSLVDMARPLINRASEQDCEGLADAKMNNGYDREEMARVACAAACVRRHSARRPR 570
541 MSQIVALEGNVSLDNEGMRGQSNVSYSGGSTDYDSQYMEDMKFRKMGALGTQY 600
571 MSQIVALEGNVSLDNEGMRGQSNVSYSGGSTDYDSQYMEDMKFRKMGALGTQY 630
601 NATGEYSNPTSDYGLYPSGSSSGQTTREMEMGKIKRTGOGYSGPSL 647
631 NATGEYSNPTSDYGLYPSGSSSGQTTREMEMGKIKRTGOGYSGPSL 677

RESULT 4
US-10-086-464-11
; Sequence 11, Application US/10086464
; Publication No. US20020199218A1
; GENERAL INFORMATION:
; APPLICANT: GORING, Daphne R. et al.
; TITLE OF INVENTION: PROLINE-RICH EXTENSIN-LIKE RECEPTOR KINASES
; FILE REFERENCE: P 25,762-A USA
; CURRENT APPLICATION NUMBER: US/10/086,464
; CURRENT FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 10/069,304
; PRIOR FILING DATE: 2002-02-19
; PRIOR APPLICATION NUMBER: PCT/CA00/00966
; PRIOR FILING DATE: 2000-08-18
; PRIOR APPLICATION NUMBER: US 60/149,466
; PRIOR FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: US 60/159,122
; PRIOR FILING DATE: 1999-10-13
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 633
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-086-464-11

Query Match 50.6%; Score 1748.5; DB 9; Length 633;
Best Local Similarity 56.8%; Pred. No. 6.5e-69;
Matches 363; Conservative 78; Mismatches 151; Indels 47; Gaps 15;
3 SAPSPGTCGPPSPSTTTTPPASAPPTTPSPSPSTPTPTSPSPSRSTPSAPPPS 62
7 SAPTNTSSPPSPSTNTSSP---PAPSPSTTPGDCSSSPSPSTIPSPAPQAFN 63
63 PPTPTGSPPLPQSPAPPTTPGSPAPVPTPTTRNPPSPVPGPPSPNPSRGGSPR--P 120

54 PPN-SSNNSPSPSPSGGGERGNGNGNDTPPRGSPSPS---PPSRNGNDNGSRSSP 119
121 PS-----SPSPSPS---SSDG-----LSTGVVGIAGVALLVIVTLICLLCKKKRR 165
151 PGDTGSGRSDNPPSSGSGGGGGRSNTNTAIIVGLVGEALLMIVLIVLCRRKKKKR 179
181 RDEEDAYVPPPPPPGPKAGGP---YGGQOQWROONATPPSDHVVITSLPPPKAPSPR 222
211 ---DSFY-----PEPMKNGOYTYGNNNNNNAQONY---PNWHLNSQGNQOQSTGGWGG 227
223 QPPPPPPPPPEMSSSG--GSDYS--DRPVLPPSPGLVLFSGSKSTTYEELARATNGFSEA 278
228 GGPSPPPPPRPTSGSDSMYSGPRPVLPPSPALALGFNFKSTITYQELAAATGFTDA 287
279 NLLGSGGFGYVHKVLPSPGKEVAVKQLKVGSGGGEREFQAEVEIISRVHRLVSLVGYC 338
288 NLLGSGGFGYVHKVLPSPGKEVAVKSLKAGSGGGEREFQAEVDIISRVHRLVSLVGYC 347
339 IAGAKRLIYFEPYNNLEHLHGEGRPTMEWSTRLKIALGSAKLSYLHEDCNPKIIHR 398
348 IADQRMILYFEPVNPKTLEYHLHGKLPVMEFSTRLIALGAAGKGLVHEDCHPRIIHR 407
399 DIKASNILDCKFEAKVADFLAKTASDNTHTVSTVMGTFCGLAPEYAAAGKLTGKSDV 458
408 DIKASNILDCKFEAKVADFLAKLTSDNTHTVSTVMGTFCGLAPEYAAAGKLTGKSDV 467
459 FSGVVLLELITGRPPVDANNVYVDDSLVDMARPLINRASEQDCEGLADAKMNNGYDRE 518
468 FSGVVLLELITGRPPVD--NSITMDTLVDNARPLMARALEDGNFELADARLEGNYPQ 526
519 EMARVACAAACVRRHSARRPRMSQIVALEGNVSLDNEGMRGQSNVSYSGGSTDY 578
527 EMARVACAAASIRHSGKRPKNQIVRALEGEVSLDALNEGKVPKPGHSNVYGLGASDY 586
579 DSSQTNEDMKFRKMGALGTQY---NATGEYSNPTSDY 614
587 SQTSYNADMKFRQIALSSQEEFVSDCEGTSNDSRDNG 625

RESULT 5
US-10-086-464-14
; Sequence 14, Application US/10086464
; Publication No. US20020199218A1
; GENERAL INFORMATION:
; APPLICANT: GORING, Daphne R. et al.
; TITLE OF INVENTION: PROLINE-RICH EXTENSIN-LIKE RECEPTOR KINASES
; FILE REFERENCE: P 25,762-A USA
; CURRENT APPLICATION NUMBER: US/10/086,464
; CURRENT FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 10/069,304
; PRIOR FILING DATE: 2002-02-19
; PRIOR APPLICATION NUMBER: PCT/CA00/00966
; PRIOR FILING DATE: 2000-08-18
; PRIOR APPLICATION NUMBER: US 60/149,466
; PRIOR FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: US 60/159,122
; PRIOR FILING DATE: 1999-10-13
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
; LENGTH: 674
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-086-464-14

Query Match 48.9%; Score 1687; DB 9; Length 674;
Best Local Similarity 51.8%; Pred. No. 3.2e-66;
Matches 368; Conservative 87; Mismatches 142; Indels 114; Gaps 25;
1 MSSAPGTCGPPSPSTTTTPPASAPPTTPSPSPSTPTPTSPSPSRSTPSAPPPS 60
6 VDSSPAPET-SNCTTPSNGIS---PSNESFPPTSPSPSPSS---ISAPPDISASFSPP 58


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; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 17
; LENGTH: 731
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-086-464-17

Query Match      40.58; Score 1399; DB 9; Length 731;
Best Local Similarity 47.38; Pred. No. 1e-53;
Matches 317; Conservative 71; Mismatches 181; Indels 101; Gaps 19;

QY 1 MSSAPSGCTGSPS---PPSNSTTTTTPRASAP---PPTPSSPPPTPTPTSPBSSR 53
Db 114 LPAKPSPPSPSPSEVPPGN--TISPPRLSESTPPVNTASPPPPS-----PPRRR 165
QY 54 S--TPSAPP---SPPPPS--TPGSPFLPQSPAPPTTPGSPAPVPTPTIRNPPSPV- 105
Db 166 SGPKPSEFPPIGNSPPNPSPNIESLPETSPPKPPLSTTFP--PSSSTPPPKKSPAATL 223
QY 106 -----GPPSPREGSGSPSPSPSPSPSPSDGLST-----GVVV 140
Db 224 PFTGPAGLDGTVVAPPIGVIEKTPSAESISPGTQPQVLVFKSLPTTTFHRSAGFLF 283
QY 141 GIAIGGVALLVITLCLCKKRRR--DEEDAYVPPPPPPGPKAGGPGGQQQWRQQ 198
Db 284 GGVIAGALLILLGLLFVFRATERNNNSSSAHHQSKTP-----SKVQHIRGG 332
QY 199 NATPPSDHVTSLPPPKKAPSPRPQPPPPPPMSSSGSDSDRVLPPSPGLVLGF 258
Db 333 NAGTNQAHVIT-MPPPTIAK-----YLSGGCDTKEN-----NSVAKNISM 372
QY 259 SKSTFYEEELARATNGFSEANLLGGGFGVYHKGVLPSGKEVAVKOLKVGSGGGEREQ 318
Db 373 PSCMFSEELSKATGSEENLLGEGFGYHKGVLKANGTEVAVKQLKIGSYGGEREQ 432
QY 319 EVELISRVHRLVSLVGYCIAGAKRLLYEFVFNNNLEHLHGEGRPTMWSRLKIAL 378
Db 433 EVDTISRVHKLHVLVGYGVNGDKRLLYEYFVKDILEFHLHENRSGVLEWEMRLIATV 492
QY 379 GSAKGLSYLHEDCNPKIIHROIKASNLIDFKFAKVADFLAKIASDTN---THVSTRV 435
Db 493 GAAKGLAYLHEDCSPTIIHROIKANILDSKEAKVSDFLAKFFSDTNSFTHISTRV 552
QY 436 MGFPGYLAPYAAAGKITEKSDVSEFSGVLELITGRPPVDANNVYDDSLVDWARPLN 495
Db 553 VGFEGYMAPYASSEKVTDKSDYSFSGVLELITGRPSIFAKDSSTNQSLVDWARPLT 612
QY 496 RASEQGDFFGLADAKMNGDYDEEMARVYACAAACVRSARRPRMSQIVRALEGNYSL 555
Db 613 KAISGESDFLVDRLKNDYDTOMANMAACAAACIROSALWRPMSQVVRALGEVALR 672
QY 556 DLNEGHRPGOSNYVSGSDYDSDSOYNEDMKFKRMAALGTQBYNATGEYSNPTSDYGL 615
Db 673 KVBE-----TGNSTVYSSSENPNDI-TPRYGTNKRFF-----DTGSSDGYTSEYGV 717
QY 616 YPSGSSSEHQ 625
Db 718 NPSQSSSEHQ 727

RESULT 8
US-10-101-464A-76
; Sequence 76, Application US/10101464A
; Publication No. US20030046728A1
; GENERAL INFORMATION:
; APPLICANT: Strabala, Timothy
; APPLICANT: Nieuwenhuizen, Nicolaas
; APPLICANT: Higgins, Colleen M.
; TITLE OF INVENTION: Compositions Isolated from Plant Cells
; TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signaling
; FILE REFERENCE: 11000.1020c2
; CURRENT APPLICATION NUMBER: US/101.464A
; PRIOR FILING DATE: 2002-03-18
; PRIOR APPLICATION NUMBER: 09/704,302

; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 17
; LENGTH: 731
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-086-464-17

Query Match      21.9%; Score 754.5; DB 9; Length 968;
Best Local Similarity 35.38; Pred. No. 1.1e-25;
Matches 184; Conservative 89; Mismatches 133; Indels 115; Gaps 16;

QY 118 PRPSSP-----SP---PSPSDGLSTGVVGIATGGVALLVIVTILCLCKKRRRDEE 169
Db 533 PPKPGEPPYFTASPAFPDNGTALSKGVIVGIAIGTVLVGLVGLYAIRKRAEK 592
QY 170 DAYVYPP-PPPGPKAGGPGGQQQWRQQNATPPSDHVTSLPPPKAPSPRPQPP 225
Db 593 -ALSERPFASWAPSGKDSGGAPQLKGAR----- 621
QY 226 PPPPPPMSSSGSDYSDRPVLPSPGLVLGFSKSTFTYEELARATNGFSEANLLGGG 285
Db 622 -----PSYDELKRCNTNFSNDELFGG 644
QY 286 PGYVHKGLVPSGKEVAVKOLKVGSGGEREQAEVEIISRVHRLHLSVGVYCIAGAKRL 345
Db 645 YGKTVRGVLPDGHILAIKRAQQSGMGATEFTEIETELLRSVHKKNLVGLIGFCFQGEOM 704
QY 346 LVSEVPANNLEHLHGEGRPTMWSRLKIALGSAKGLSYLHEDCNPKIIHROIKASNI 405
Db 705 LVETPMGTTRDSITGSGIYLDWKRLRLALGSARGLAYLHLEANPPIIHRDVKSTNI 764
QY 406 LIDKFEKAVADFGLAKIASDTNT--HVSTRVNGIFGYLAPEYAAAGKITEKSDVSEFV 464
Db 765 LLDHLTAKVADFGLSKLVSDSGKHVSQVKGILGYLDPEYMSQQLTEKSDVSEFV 824
QY 465 LLELITGRPPVDANNVYDDSLVDWARPLNASEQGFEG---LADAKMNN-GYDREEM 520
Db 825 MLELITAKOPTIEKGYVYRE-----IRTAMDKNDQ--DYGYVREMDPMSRSMGY-LVGF 876
QY 521 ARMVACAAACVRSARRPRMSQIVRALEGVNSLDNEGMRPGOSNYVSGSDYSDYDS 580
Db 877 SRFLDLAMRCYERESADPTMSEVVKALETMLQ-----NDGHTNITSASSS---ATDFGS 929
QY 581 SQ-----YNEDMKFKRMAALGTQBYNATGEYSNPTSDYGL 615
Db 930 TKGAPRHPYNDALPK-----KEYSYSDSFDYS---GGYGL 961

RESULT 9
US-10-101-464A-71
; Sequence 71, Application US/10101464A
; Publication No. US20030046728A1
; GENERAL INFORMATION:
; APPLICANT: Strabala, Timothy
; APPLICANT: Nieuwenhuizen, Nicolaas
; APPLICANT: Higgins, Colleen M.
; TITLE OF INVENTION: Compositions Isolated from Plant Cells
; TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signaling
; FILE REFERENCE: 11000.1020c2
; CURRENT APPLICATION NUMBER: US/101.464A
; PRIOR FILING DATE: 2002-03-18
; PRIOR APPLICATION NUMBER: 09/704,302
```

```
; PRIOR APPLICATION NUMBER: 09/228,986
; PRIOR FILING DATE: 1999-01-12
; PRIOR APPLICATION NUMBER: 60/162,866
; PRIOR FILING DATE: 1999-11-01
; PRIOR APPLICATION NUMBER: PCT/US00/00724
; PRIOR FILING DATE: 2000-01-11
; NUMBER OF SEQ ID NOS: 989
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 71
; LENGTH: 630
; TYPE: PRT
; ORGANISM: Pinus radiata
; US-10-101-464A-71

Query Match      21.3%; Score 736; DB 9; Length 630;
Best Local Similarity 37.2%; Pred. No. 4.8e-25;
Matches 175; Conservative 68; Mismatches 125; Indels 102; Gaps 12;

QY 90 PAPVTPTRNPPSVGPP---SNPSREGSPRPSPSPSPSSDGLSTGVVVGIAIGG 146
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 208 PCGSPSPFPFPFPFPFPFPFPFPFPFPFPFPFPFPFPFPFPFPFPFPFP 251
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 147 VALLIVITLCLLCKKKRDEEDAYVPPPPKAGPGYGGQQQQOQOQOQOQOQO 206
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 252 AALLF-----AAPAIGFAW-----WRRK---POEH 274
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 207 VVTSLPPPKAPSPRQPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPP 266
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 275 -----FEDVPA--BEDPEVHLGQLK-RPSLR 297
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 267 ELARATNGSEANLLQGGGYYHKGVLPSGKEVAVKOLK-VSGGQGEREFOAEV 325
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 298 ELQVATDGSNNRILGSGFYKGRGLADGSLVAVKRLKEERTPGGELQFOTEV 357
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 326 VHRHLVSLVGYCIAGAKRLVVEFPNNLE--LHLHGGRPTMESTRIKALGSA 383
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 358 AVHNRLLRGFCMTTERLLVVPYANGSVASCLREARQNDPLDPTTKRIALGS 417
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 384 LSYLHEDCNPKIIRDIKASNILIDFKFEAKVADFLAKIASDTNTHVSTRVMT 443
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 418 LSYLHEDCNPKIIRHVDYKAANILLDEYEAUVGDFGLAKLMDYKDHVTTAV 477
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 444 PEYASGKTEKSDVSFGVILELITGRPVJANNYYVDDS--LYDWARPLNRA 501
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 478 PEYLSGKSEKSDVFGYIGMLLELITGQRAFLARLANDDDVMLLDWVKGL 533
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 502 DEGLADAKMNNYDREEMARMVACAAACVRRHSARRRPRMSQIVRALEGN 551
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 534 RLDMLVDPLKNNYVAEVPEQLLOVALLCTQGSFMDPRPKMSEVVRMLEGD 583
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 10
US-09-828-313-27
; Sequence 27, Application US/09828313
; Patent No. US20020059662A1
; GENERAL INFORMATION:
; APPLICANT: COSTA e SILVA, OSWALDO DA
; APPLICANT: BOHNERT, HANS J.
; APPLICANT: THIELEN, NOCHA VAN
; APPLICANT: CHEN, ROUYING
; APPLICANT: SARRIA-MILLAN, RODRIGO
; TITLE OF INVENTION: PROTEIN KINASE STRESS-RELATED PROTEINS AND METHODS OF
; TITLE OF INVENTION: USE IN PLANTS
; FILE REFERENCE: 16313-0032
; CURRENT APPLICATION NUMBER: US/09/828,313
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: 60/196,001
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 128
; SOFTWARE: Patent Ver. 2.1
; SEQ ID NO 27
; LENGTH: 749
; TYPE: PRT

; ORGANISM: Physcomitrella patens
; US-09-828-313-27

Query Match      20.9%; Score 722; DB 10; Length 749;
Best Local Similarity 35.6%; Pred. No. 2.3e-24;
Matches 177; Conservative 76; Mismatches 160; Indels 84; Gaps 15;

QY 100 PPSVPGPPSPNPSREGSPRPSPSPSPSPSSDGLSTGVVVGIAIGGVALIVITL-TCL 158
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 259 PPPPAGTTP-----APRTPSPGTSNGSSSHLPLGAILGIAAGGAVLELLALGICL 310
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 159 LCXKKRRR---DEEDAYVPPP---PPGPKAGGP-----YGGQQOQOQOQOQO 199
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 311 CCRKRSKKALGDPEATTSSRRPWTPTPLSAKQSDPSKSIDTKTKRNIFGSSKSEKKS-- 368
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 200 ATPSPDHWVTSLLPPPK--APSPRPQPPPP-----PPPPFMSSSGGSDYSDRPVLP 252
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 369 ----SKRVFEPAPLDKGADEPVVKASPPYKVLKAPSPFKGIS----- 408
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 253 GLVLGFSKST-----FTYEELARAINGFSEANLLGOGGFGYVHKVLPSSKE 299
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 409 GLGAGHAKATIGKYNKSNIAATPFSVADLQAATNFSQDNLIGSGMGRVTRAEFPNGQV 468
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 300 VAVKOLKVGSS--QGEREFOAEVILSRVHRHESVLYGYCIAGAKRLVVEFPNNLE 357
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 469 LAVKIDSSASMWQNEDDFLSVDSLARLQAHNTAEVLVGYCIEHQDRELLAYEYVSRGTLN 528
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 358 --LHLHGGRPTMESTRIKALGSAKLSLHEDCNPKIIRHDIKASNILIDFKFEAKV 415
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 529 ELLHSGENTKALSMNVRIKALGSALELYLHEVCAPPVYVHNEKFSANILLDDDELNPVH 588
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 416 ADFGLAKIA-SDTNTHVSTRVMTGTFGLAPYAAAGKTEKSDVSFGVILELITGR 474
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 589 SDGLAALAPSGSERQVSAQMLGSEFGYSAPEYASGITYTVKSDYVSGVWMLLELTGRKS 648
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 475 VDANNVYVDSLVYDWARPLNRASEQQDFEGIA---DAKMNGYDREEMARMVACAAACV 531
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 649 LDSRPRSEQSLVRWATPQLH-----DIDALARWVDSLAKGYPAKSLSRFADIVLCV 702
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 532 RHSARRRPRMSQIVRAL 548
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 703 QPEPEFRPPKSEVVQAL 719
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 11
US-10-101-464A-927
; Sequence 927, Application US/10101464A
; Publication No. US20030046728A1
; GENERAL INFORMATION:
; APPLICANT: Strabala, Timothy
; APPLICANT: Nieuwenhuizen, Nicolaas
; APPLICANT: Higgins, Colleen M.
; TITLE OF INVENTION: Compositions Isolated from Plant Cells
; TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signaling
; FILE REFERENCE: 11000.1020C2
; CURRENT APPLICATION NUMBER: US/10/101,464A
; CURRENT FILING DATE: 2002-03-18
; PRIOR APPLICATION NUMBER: 09/704,302
; PRIOR FILING DATE: 2000-11-01
; PRIOR APPLICATION NUMBER: 09/228,986
; PRIOR FILING DATE: 1999-01-12
; PRIOR APPLICATION NUMBER: 60/162,866
; PRIOR FILING DATE: 1999-11-01
; PRIOR APPLICATION NUMBER: PCT/US00/00724
; NUMBER OF SEQ ID NOS: 989
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 927
; LENGTH: 629
; TYPE: PRT
; ORGANISM: Eucalyptus grandis
; US-10-101-464A-927
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Query Match          20.48; Score 704.5; DB 9; Length 629;
Best Local Similarity 41.88; Pred. No. 1.1e-23;
Matches 151; Conservative 71; Mismatches 92; Indels 47; Gaps 8;

QY 263 FYVEELARATNGFSEANLGGGGYVHKGLPSGKEVAVKOLK---VGSQGERERQA 318
DB 297 FHFRELQIARNSTSSKNILGKGFGHVKGLVQDGLTAVAKDAKAVG---GEIQFOT 353
QY 319 EVELISRVHRLVSLVGYCIAGAKRLIYEFVFNNNLELHGHGEGPTMEWSTRLKIAL 378
DB 354 EIEIMISLAVHRLRLYGFCTPAEKLIIYFPMGNGSVASRL--KGRPLVDGWTCKRIAL 411
QY 379 GSAKGLSYLHEDCNPKIHRDIKASNLILDFKFAKVADFGIAKIASDTNTHVSTRVGT 438
DB 412 GAAGGLYLHEDQCPKIHROVKAAANLEDDYCEAVVGDFGLAKLLEHQQDSHVTAVRG 471
QY 439 FGVLAPYAAAGSKLTKSDVFSFGVWLELITGRPVYD---ANNVYVDDSLVDWARPLL 494
DB 472 VGHIAPEYLTSGQSEKTDVFGGILLLELTGQRALEFGKAAQ---KGMILDWK--- 525
QY 495 NRASEQDDEGLADAKNNGYDREEMARVACAAACVHKSARRPRMSQIVRALGNVSL 554
DB 526 -KHOEKKLEMLVDKOLRSNYDRIELEIVQVALLCTQYLPFAHRPKMSEVVRMLEGD--- 581
QY 555 SDLNEGRPGOSNYSSYGGSTDYSSOYNEDMKKFKMALGTQYKATGEYSNPTSDYG 614
DB 582 -----GLAERMEASORVESNKG-----KPEHSSSDRYSLTDSDS 617
QY 615 L 615
DB 618 L 618

RESULT 12
US-10-101-464A-80
; Sequence 80, Application US/10101464A
; Publication No. US20030046728A1
; GENERAL INFORMATION:
; APPLICANT: Strabala, Timothy
; APPLICANT: Nieuwenhuizen, Nicolaas
; APPLICANT: Higgins, Colleen M.
; TITLE OF INVENTION: Compositions Isolated from Plant Cells
; TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signaling
; FILE REFERENCE: 1:000.1020c2
; CURRENT APPLICATION NUMBER: US/10/101.464A
; CURRENT FILING DATE: 2002-03-18
; PRIOR APPLICATION NUMBER: 09/704,302
; PRIOR FILING DATE: 2000-11-01
; PRIOR APPLICATION NUMBER: 09/228,986
; PRIOR FILING DATE: 1999-01-12
; PRIOR APPLICATION NUMBER: 60/162,866
; PRIOR FILING DATE: 1999-11-01
; PRIOR APPLICATION NUMBER: PCT/US00/00724
; PRIOR FILING DATE: 2000-01-11
; NUMBER OF SEQ ID NOS: 989
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 80
; LENGTH: 707
; TYPE: PRT
; ORGANISM: Pinus radiata
US-10-101-464A-80

Query Match          20.48; Score 703.5; DB 9; Length 707;
Best Local Similarity 34.08; Pred. No. 1.4e-23;
Matches 178; Conservative 81; Mismatches 179; Indels 85; Gaps 14;

QY 84 TTPGSPAPYTPTRNPPSPVPGPSPPREGSPSPSPS--PPSPSDG-----L 134
DB 247 TGRAPPPPTTPP-----PPSN-----NRPKSNVVPSSGGSGGNSNNKSL 289
QY 135 STGVVWGIAIGGVALLVITLCLCKKKRRRDEDAYVYPPPPPGPKAGPYGGQOQ 194
DB 290 SSGAIVGIIFAVILTVVAAILGVILYARKSPREDD-----BEKL 329
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QY 135 WRQQNATP--PSDHVVTISLPPPKAPSPRPPPPPPPPPPPMSSSG-----GSDYSRDPVL 247
DB 330 SNRVFTPLSPDAELLKESPEQKYSSSPLEIALKPPPPSERNKSTGDKGFGSIFSSKRTK 389
QY 248 PPPSPGLVLPFSKSTFTYEELARATNGFSEANLGGGGYVHKGLPSGKEVAVKOLK 307
DB 390 NP-----ISATYSIADLQVATNSFQDNLIAPGALGRYAEFPGKILAVKKLDT 441
QY 308 G--SQGGEREFOAEVIELISRVHRLVSLVGYCIAGAKRLIYEFVFNNNLELHGHG 363
DB 442 STLSLQREDFDLDAVSNISRLHHPNITELVGYCTHEQVLLVYFEDNSGLVDLHMADE 501
QY 364 GRPTMEKSTRUKIALGSAKGLSTLHEDCNPKIHRDIKASNLILDFKFAKVADFGIAK 423
DB 502 TTRNLSSLIRVKIALGSAVLETLHEVCSPTVHKKFKSSNILLDDDFNPLSDCGIA-- 559
QY 424 ASDTNHSTRVNGYFGYLAPYAAAGSKLTKSDVFSFGVWLELITGRPVYD 493
DB 550 ALNPSEERQVQVIGSGFGISAPYVSGIYTKMSDVISFGVWLELITGRPKPJDSSTRSE 619
QY 484 DSLVOWARPLNRASEQDDEGLA---DAKMNNGYDREEMARVACAAACVHKSARRPR 540
DB 620 QSLVSWATPQLH-----DIDALAKMVDPALAGSYPAKSLSRFADIIALCIQPEPERPP 673
QY 541 MSQIVRALGNVSLSDLNEGRPGOSNYSSYGGSTDYSSOY 583
DB 674 MSEVVOALVRMQRASLAKRMTGDE-----IADHPADY 707

RESULT 13
US-10-101-464A-74
; Sequence 74, Application US/10101464A
; Publication No. US20030046728A1
; GENERAL INFORMATION:
; APPLICANT: Strabala, Timothy
; APPLICANT: Nieuwenhuizen, Nicolaas
; APPLICANT: Higgins, Colleen M.
; TITLE OF INVENTION: Compositions Isolated from Plant Cells
; TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signaling
; FILE REFERENCE: 110CQ.1020c2
; CURRENT APPLICATION NUMBER: US/10/101.464A
; CURRENT FILING DATE: 2002-03-18
; PRIOR APPLICATION NUMBER: 09/704,302
; PRIOR FILING DATE: 2000-11-01
; PRIOR APPLICATION NUMBER: 09/228,986
; PRIOR FILING DATE: 1999-01-12
; PRIOR APPLICATION NUMBER: 60/162,866
; PRIOR FILING DATE: 1999-11-01
; PRIOR APPLICATION NUMBER: PCT/US00/00724
; PRIOR FILING DATE: 2000-01-11
; NUMBER OF SEQ ID NOS: 989
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 74
; LENGTH: 638
; TYPE: PRT
; ORGANISM: Pinus radiata
US-10-101-464A-74

Query Match          19.64; Score 678; DB 9; Length 638;
Best Local Similarity 43.18; Pred. No. 1.6e-22;
Matches 147; Conservative 68; Mismatches 104; Indels 22; Gaps 8;

QY 254 IVLGFSKSTFTYEELARATNGFSEANLGGGGYVHKGLPSGKEVAVKOLKVGSG 312
DB 295 ICLGHLX-RFSFKELRVSTNNFNSSNIIILGVGYVYKGLQDGTIVAIIKRLKDNVGG 353
QY 313 ERFQAEVIELISRVHRLVSLVGYCIAGAKRLIYEFVFNNNLELHGHGEGPTMEW 370
DB 354 EIQFQTEVEMISLAVHRLRLYGFCTTSRRLIYPTYPNGSVASCLRDHNGKIALDW 413
QY 371 STRUKIALGSAKGLSTLHEDCNPKIHRDIKASNLILDFKFAKVADFGIAKIASDTN 430
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Db 414 PTRKRIALGAARGLLYLHBCQDPKIIHRDVKAANILLDEYFEAVVGFGLAKLLDHRDHS 473
Qy 431 VSTRVMTGFGYLAPEYASGKLTSEKSDVFSFGVWLELITGTRPVD-----ANNVTVDSL 486
Db 474 VTTAVRGVGHIAPEYLSGTSGSEKTDVFGGILLITGQALDFQAAKQKV---M 530
Qy 487 VDWARPLNRASGDFEGLADAKMNNNGYDREEMARMVACAAACVHRHSARRRPMQSVLR 546
Db 531 LDWVKKL----HQSKLLHLLADKLGKGNFORVELEEMVQVSLCTQFGPGRPKMCDVLR 586
Qy 547 ALEGNVSLDLNEGMRPQSNVYS-----SYGSGTDYDSS 581.
Db 587 MLEGD-GLTERWEIIZQKIETPRYRVTELPITYSELVEEDSS 626

RESULT 14
US-10-101-464A-812
; Sequence 812, Application US/10101464A
; Publication No. US20030046728A1
; GENERAL INFORMATION:
; APPLICANT: Strabala, Timothy
; APPLICANT: Nieuwenhuizen, Nicolaas
; TITLE OF INVENTION: Compositions Isolated from Plant Cells
; TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signaling
; FILE REFERENCE: 11000.1020C2
; CURRENT APPLICATION NUMBER: US/101/101.464A
; PRIOR FILING DATE: 2002-03-18
; PRIOR APPLICATION NUMBER: 09/704,302
; PRIOR FILING DATE: 2000-11-01
; PRIOR FILING DATE: 1999-01-12
; PRIOR FILING DATE: 1999-11-01
; PRIOR FILING DATE: 2000-01-11
; NUMBER OF SEQ ID NOS: 989
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 812
; LENGTH: 523
; TYPE: PRT
; ORGANISM: Eucalyptus grandis
US-10-101-464A-812

Query Match 19.5%; Score 672; DB 9; Length 623;
Best Local Similarity 40.2%; Pred. No. 2.8e-22;
Matches 144; Conservative 70; Mismatches 104; Indels 40; Gaps 7;

Qy 263 FTYELARATNGFSEANLLGGGFGYVHKGVLPSCKEVAVKQLK-VGSGGGEREQAEVE 321
Db 290 FHFRELANATNFGSKNLIGRGGSHVYRGCLSDGMVVAIKRLNRVVDALGGDVQPTLR 349
Qy 322 IISRVHRHLVSLGYCIAGAKRLLVYEFVPPNNLEHLHGEGRPTMEWSTRLKALGSA 381
Db 350 MISLAVHRLNLLRFGCMQTERLLVYPYNGSVAFRL--RAKPTLEWSTKRKIALGAA 407
Qy 382 KGLSYLHEDCNPKTIHRDIKASNTLIDFKFAKVADEGLAKIASDTNTHVSTRVMTGFGY 441
Db 408 RGLLYLHEQCQDPKTIHRDVKAANILLDDYCEAVVDFGLAKLLDBRESHVTTAVRGTAGH 467
Qy 442 LAPEYASGKLTSEKSDVFSFGVWLELITGTRPVD-----ANNVTVDSLVTDWARPLNRA 497
Db 468 IAPYLLSGSSSEKTDVFGGILLITGLRALFEFGKAANO---RGAMLDVVR----KV 520
Qy 438 SEQGDFEGLADAKMNNNGYDREEMARMVACAAACVHRHSARRRPMQSVLRVRALEGNVSLDL 557
Db 521 HLEKKIEVLVDKDKONDRLEIEIITQVSLCTQYLPTRPKMSEVVVRMLEGD----- 574
Qy 558 NEGMRPQSNVYSYSGSTDYDSSQYNDKMKFKKMAIGTQYNTAGTSEYNSPTSYGL 615
Db 575 -----GLVERWEASQRAESTR-----CRAANEFSSESYSLDIODSSL 612

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RESULT 15
US-10-219-220-263
; Sequence 263, Application US/10219220
; Publication No. US20030082724A1
; GENERAL INFORMATION:
; APPLICANT: Flinn, Barry
; APPLICANT: Lasham, Annette
; TITLE OF INVENTION: Compositions affecting programmed cell
; TITLE OF INVENTION: death and their use in the modification of plant development
; FILE REFERENCE: 11000.1022C1
; CURRENT APPLICATION NUMBER: US/10/219,220
; CURRENT FILING DATE: 2002-08-14
; PRIOR FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 290
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 263
; LENGTH: 366
; TYPE: PRT
; ORGANISM: Pinus radiata
US-10-219-220-263

Query Match 19.1%; Score 661; DB 9; Length 366;
Best Local Similarity 43.1%; Pred. No. 5.2e-22;
Matches 141; Conservative 57; Mismatches 107; Indels 22; Gaps 5;

Qy 232 FMSSGGSDYSDRPVLPPLPPGVLGFSKSTFTYELARATNGFSEANLLGGGFGYVHK 291
Db 37 YKSEGAKEGPPQKTIAPALSL-----BELKEATNGEAKALIGSGSYGRVY 87
Qy 292 GVLPSGKEVAVKQLKVGSGGGEREQAEVEIISRVHRHLVSLGYCIAGAKRLVYEF 350
Db 88 AMLSDGQPAAIKKLDVNSOPNESEFLAQISMVSRLLKHDHIVELVGYCVGEGTLRVLAYEF 147
Qy 351 VPNNLEHLHG-----EGRPTMEKSTRKIALGSAKGLSYLHEDCNPKTIHRDIKAS 403
Db 148 ATMGSLHDILHGRKGQGAQPGVLDWMQVRKIAVGAAGLEYLEHKEVQPHIHRDIRS 207
Qy 404 NILIDFKFAKVADFGAKIASDTNTHV--STRVMTGFGYLAPEYASGKLTSEKSDVFSFG 462
Db 206 NVLLFDDFKAKIADFNLSNQAPDMAARLHSTVLTGFGYHAFYANTGQITOKSDVYSFG 267
Qy 463 VVLELITGRRPVDANNVTVDSLVTDWARPLNRASEQGDFEGLADAKMNNNGYDREEMAR 522
Db 268 VVLELLTGKKEPVDHTMPRGQOSLVTWATPRLS----EDKVKQCVDPKLGEPYPPKAVAK 323
Qy 523 NVACAAACVHRHSARRRPMQSVLRVRALE 549
Db 324 LAVAALCVQYEADEFNPNMSIIVKALQ 350

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Search completed: July 2, 2003, 15:20:53
Job time : 37 secs


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QY      299 EVAYKQLVKGSGGGEREQAEVEIISRYHHRLHSLVGYCI-AGAKRLLWVEYFVNMMLE 357
Db      360 EIAVLKSKAGSGGGEREQAEVEIISRYHHRLHSLVGYCSNAGGQRLIVTFEFLNDTLE 419
QY      358 LHLHGEGRPMTMEWTRFKIALGSAGLSYLBEDCNPKIIHRDIKASNILIDFKPEAKVAD 417
Db      420 FHLHGKSGTYMDWPTLTKIALGSAGKLAYLHEDCHPKIIRHDIKASNTLLDINFPAKVAD 479
QY      418 FGLAKIASDTNTHYSTRVMGTFGYLAIFYAASGKLITEKSDVFSGVWLLELITGRPPVDA 477
Db      480 FGLAKLGSDNNHTHSTRVMGTFGYLAIFYAASGKLITEKSDVFSGVWLLELITGRPPVDL 539
QY      478 NNVTYVDSLVDWARPLLMKRASEQDDFEGLADAKMNGNYDEEMARMWVACAAACVRRHSARR 537
Db      540 SG-DMEDSLVDWARPLCMRVQAQGEYSELVDPFLEHQHYEPYEMARMWVACAAAARHSGR 598
QY      538 RPRMSQTVRALEGNVSLDLNEGMRPGSNVSYSGSSTDYDSQYNEDMKKPRMALGT 597
Db      599 RPRMSQVRLTEGDASLDLDDGVKKPOSS--SGEGSSDYEMGTGYGAEMEKFRKVTLES 656
QY      598 QENATCEYSNPSTDYGLYPSSSGSGQTREMELWG----KIKRTGGQ 641
Db      657 RDYGASSEY-GATSEYGLDPSSSSE-----EMHIGGSTSKTTINRG 698

RESULT 3
T05264
Probable serine/threonine-specific protein kinase (EC 2.7.1.1-) T4L20.20 - Arabidopsis;
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 17-Mar-2000
C:Accession: T05264
R:Bevan, M.; Terry, N.; Ardiles, W.; Buysshaert, C.; Dasseville, R.; De Clerck, R.;
ewes, H.W.; Mayer, K.F.X.; Schueller, C.
submitted to the Protein Sequence Database, September 1998
A:Reference number: Z15406
A:Accession: T05264
A:Molecule type: DNA
A:Residues: 1-674 <BEV>
A:Cross-references: EMBL:ALJ023094
A:Experimental source: cultivar Columbia; BAC clone T4L20
C:Genetics:
A:Map position: 4
A:Introns: 180/1; 221/1; 381/1; 421/1; 444/3; 470/2; 518/3; 583/3
A>Note: T4L20.20
C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase hor
C:Keywords: phosphotransferase; protein kinase

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[illegible][illegible]

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Db 272 -AATLGHNSQSTFTYDELSTIATEGFAQSNLLGGGFGVHKGVLPSGKEVAVKSLKSGG 330
QY 312 GEREFQAEVLIISRVHRLHSLVGVCIAGAKRLLYTEFPNNMLEHLHGEGRPTMWS 371
Db 331 GEREFQAEVDIISRVHRLHSLVGVCIISGQKLLVTEFIPNNLFEHLHGKGRPVLDWP 390
QY 372 TRKIALGSAKGSYLHEDC-----NPKIHRDIKASNILLIDKFEAKVADPGL 420
Db 391 TRYKIALGSAKGSYLHEDCKKIFISHICISHPFIHRDIKASNILLIDKFEAKVADPGL 450
QY 421 AKTASDTNTHSVRVMTGTFGLAYEASGKLTESKDSVFGVVLLELITGRRPVDANNV 480
Db 451 AKLSQDNYTHSVRVMTGTFGLAYEASGKLSKDSVFGVVLLELITGRPDLDTG- 509
QY 481 YVDSLDVMDARPLNASEGDEFEGLADAKMNNGYDREEMARVACAAACVHRHARRPR 540
Db 510 EMDSLVDNARPLNCLKAAQGDYNQLADPRLNYSHOEMVOMASCAAAIRHARRPK 569
QY 541 MSQ-----IVRALGNVSLDNLNEMRPGQSNVSYSGSDIDYSSQYNEDMKK 589
Db 570 MSQVOKLIPLVGSLIVRALGSDMSDLSEGTREGQSTYLSPGSVSSEYDASSTADMKK 629
QY 590 FRKMALGTQYNATGEYSNPTSDGLYPSGSSSGQTTREMEMGKIKTGQ 640
Db 630 FKKLALENKEYQS-EYGG-TSEYGLNPSASSE-----EMNRGSMKRNPQ 673

RESULT 4
D96728
Hypothetical protein F24J13.3 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C:Accession: D96728
R:Rheologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Huizar, L.; Dewar, T.H.;
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.;
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziani,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719; PMID:11130712
A:Accession: D96728
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-710 <STO>
A:Cross-references: GB:AE005173; NID:96175155; PIDN:AAF04882.1; GSPDB:GN00141
C:Gene: F24J13.3
A:Map position: 1
```

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Query Match 43.9%; Score 1515.5; DB 2; Length 710;
Best Local Similarity 46.2%; Pred. No. 9.3e-42;
Matches 333; Conservative 81; Mismatches 158; Indels 149; Gaps 19;

QY 2 SSASP-GTGSPSPSPSNSTTTTPPA-----SAPPTTSPSPSPSTI 44
Db 27 SAPPTTDSAPPPSPADS---SPPFALPSLPAPVSPPTVSSPPPLDSSGPPPPDL 83
QY 45 PTFSPSPSPSPSPAPPP-----SPTTP-----STGSP 72
Db 84 --TPPSPSPPPAPPPPIPIVFPIDSPPESTNDEPPPEVFPPEPPPPADESPAPP 141
QY 73 PP--LPQP-----SPPATTPG-SPAPVPTPTRN-----PPPSV 104
Db 142 PPEQLPPASSPOGPKPKKHHPGATSPAPASATSPAPNAPPNRSHPALPKST 201
QY 105 P--GPSNPSREGSRPPSPSPSSDGLSTGVVVGIAIGVALLIVTILCLCK 162
Db 202 NAGGGLTSPSR--GVSPSGNSVPPPNANSGGYQCKTMAGFAIAGFAVIALMAYVELVRK 259
```

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QY 153 KRRDE--EAYTYPPP-----PPGPKAGGPGGQGGQRRQONATPPSDH 206
Db 260 KKRINDAYSCSCEIFENFSIKSDGFLYQGNPTKISGPGGYNQSQS--NSGNS----- 312
QY 207 VVTSLPPPKAFSPRQPPPPPPPMSSSGSDYSDRPVLPPLPPPGVLGFSKSTFTYE 266
Db 313 -----FGSOGGGYTRSGSAPDSA--VMGSGQTHFTYE 344
QY 267 ELARATNGFSEANLLGQGGFGVYHKGVLPSGKEVAVKQLKVGSGGGERFQAEVEIISRV 326
Db 345 ELTDTITEGFSKHNILGEGFGCVYKGLNDGKLVAVKQLKVGSGGQDRFKAEEVEIISRV 404
QY 327 HHRHLVSLVGVCIAGAKRLLYTEFPNNMLEHLHGEGRPTMWSNTRKIALGSAKGLSY 386
Db 405 HHRHLVSLVGVCIADSERLLIYVNPOTLEHHEGKGRPVLENAVRVATIGSAGKGLAY 464
QY 387 LHEDCNPKIIRHDIKASNILLIDKFEAKVADPGLAKIASDTNTHSVRVMTGTFGLAYE 446
Db 465 LHEDCNPKIIRHDIKASNILLIDDEFEQVADFLAKINDSTQTHSVRVMTGTFGLAYE 524
QY 447 AASGKLTESKDSVFGVVLLELITGRRPVDANNVDDSLVDNARPLNASEGDEFEGL 506
Db 525 AQSGKLTDRSDVFSFGVVLLELITGRKPVDQYQPLGEESLVEWARPLHKAETGDFSEL 584
QY 507 ADAKMNNGYDREEMARVACAAACVHRHARRPRMSQIVRALEGNVSLDNLNEMRPGQS 566
Db 585 VDRLEKHYVENEVFRMIETAAACVHRHSGPKPRMVVVVRAUDSGMDGIDISNGKVGUS 644
QY 567 NVYSYSGSTDYDSSQYNEDMKKFKMALGTQYNATGEYSNPTSDGLYPSGSSSGEOT 626
Db 645 SA-----YDSQYNNDMTKFKMAFGFDDSDSGMYS--GDYSVQDSRKSGNSGAS 692
QY 627 T 627
Db 693 S 693

RESULT 5
D96711
Hypothetical protein F24J5.8 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C:Accession: D96711
R:Rheologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Huizar, L.; Dewar, T.H.;
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.;
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziani,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719; PMID:11130712
A:Accession: D96711
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-708 <STO>
A:Cross-references: GB:AE005173; NID:95734709; PIDN:AAD49974.1; GSPDB:GN00141
C:Gene: F24J5.8
A:Map position: 1

Query Match 42.3%; Score 1459.5; DB 2; Length 708;
Best Local Similarity 41.8%; Pred. No. 5.5e-40;
Matches 317; Conservative 90; Mismatches 127; Indels 225; Gaps 21;

QY 1 MSSAP-----SPTGSGSPSPSPSNSTT-TTPPPASAP-PPTTP--SSPPSPSTI 48
Db 1 MATTPVQPVSNPSPPVTSPPPLNANSTAPPPVTSPLPPSPAPPPNAPPPPPPTTSP 60
QY 49 PPSRSTP-----SAPPPSPPTPSTPGSPPLPQP-----SPP--APTTP 86
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Db 61 PPVANGAPPPLPKPPSSPPQVIPSPPSTSPPPQVLPSPSPSASPPALVPELP 120
QY 87 GSPAP--VTPP-----TRNPPSV-----EGPSN-PSREGSPRPPSP-- 124
Db 121 SPPPPASVPPFRSPSPPIILVGPSPVRISQSPPPSPDRPTQSPPPSPSPSERP 180
QY 125 --SPSPSSDGLSTGVVVGIAIGVALLVITLCLCKKKRRRDEEDAYVPPPPPGP 182
Db 181 TQSPSPSPS-----ERTQSPPPSPSP-- 202
QY 183 KAGGPGGQQQWQONATPPSDHVVTLPLPPPK--APSPRQPPPPPPPPFMS-- 234
Db 203 -----SPSDRPSQSPPPPPEDIKQPPRRSPSPSPPTFSSPPSP 244
QY 235 ---SSGSDYSDRPLVPP----- 250
Db 245 EILVPGSNPNQNNETLPPDLAPNPNNSGIGTGANVGVISVAVVWTLFGIVWCIR 304
QY 251 -----SPGLV-----LQFSKST 262
Db 305 KREKRLSAVSGDVTTPSPMSSTARSDGAFFRMQSSAPVGAASKRSGSYQSGLGSKAL 364
QY 263 FTYEELARATNGFSEANLLGGGFGYHKGVLPSGKEVAVKOLKVGSGQGEREFAVEI 322
Db 365 FSYEELKATNGFSEANLLGGGFGYHKGVLPSGKEVAVKOLKVGSGQGEREFAVEI 424
QY 323 ISRVHHRHLSVGYCIAGAKRLVYFVPPNNLHLHGEGRTPMWSSTRLKALGSAK 382
Db 425 LSRHHRHLSVGYCIAGAKRLVYFVPPNNLHLHGEGRTPMWSSTRLKALGSAK 483
QY 383 GLSVLHEDCPKTIHRDIKASNILIDFKFAKADFGAKTASDNTNTHSVTMGTGYL 442
Db 484 GLAYLHEDCPKTIHRDIKASNILIDFKFAKADFGAKTASDNTNTHSVTMGTGYL 543
QY 443 APEYASGKLTESKDYVSFGVWLELITGRPDVANNVYDSDLVQWAPRLNASEQD 502
Db 544 APEYASGKLTESKDYVSFGVWLELITGRPDVANNVYDSDLVQWAPRLNASEQD 603
QY 503 FEGADAKMNGYDREMARVACAAACVHRSAARRRPMQSIQVRALEGVNSLSDNEGMR 562
Db 604 FDSLADPKLGNVYSEMFEMIAAGACVRLATKPRMGIQVRAFE-SLAEDLTNGMR 662
QY 563 PGOSVYSSYGGSDYSDSYNEDMKFRKALGTQYIN 601
Db 663 LGSEV-----FNSAQSAEIRLFRMAFGSQNYS 692

RESULT 6
F86387
probable Pto kinase interactor [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C:Accession: F86387
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Huizar, L.; Dewart, T.H.;
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719; PMID:11130712
A:Accession: F86387
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-760 <STO>
A:Cross-references: GB:AE005172; NID:g11079512; PIDN:AAE29223.1; GSPDB:GN00141
C:Genetics:
A:Map position: 1
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Query Match 41.5%; Score 1434; DB 2; Length 760;
Best Local Similarity 45.9%; Pred. No. 3.7e-39;
Matches 313; Conservative 91; Mismatches 142; Indels 136; Gaps 20;

QY 3 SAPSPGTGSPPPSPNSSTTT-----PPASAPP-----PTTPSP-PPPTSTIPT 46
Db 116 SSPPSPSPSPPPPPTEAPTITPSPPTNPPPPSPSPSPSPSPSPSPSPSPSPSPSP 175
QY 47 S-----PPSSRSTSPAPP-----PSPPSPSP-----GSPSP-- 74
Db 176 SHSPRHLPLSPASBEIPPPRHLPPPPRHLPPPPRHLPPPPRHLPPPPRHLPPPPRHL 235
QY 75 --LPSPSPAPV-----TPSPSPAPV-----TPSPSPSPSPSPSPSPSPSPSP 108
Db 236 SKRPTSPSPSPSDSKRPHVPSPPSPPEETLPPPKSPDPLPNSSSPPTLLPSSVSP 295
QY 109 SNPSREGSPSPSPSPSPSP-----SSDGLSTGVVVGIAIGVALLVITL----- 159
Db 296 SPKRKSVPSPDPN-SPNNPTPTDSSSGISIAAVGVSIG--VALVLLTLLGVVWCL 352
QY 160 CKKXRRDEEDAYVPPPPPGPKAGPGYGGQQQWQONATPPSDHVVTLPLPPPKAPS 219
Db 353 KKKKRLSTIGGYVMT-----MESSPRSDAL--LKTQSSAPL 392
QY 220 PPRQPPPPPPPFMSSSGSDYSDRPLVPPSPSPGLVGFPSKSTFYEEELARATNGFSEAN 279
Db 393 V-----GNRSSNTYLSQSTFG--GFGQSRFLFYEEELVATNGFSDEN 434
QY 280 LLGQGGFGYVHKGVLPSGKEVAVKOLKVGSGQGEREFAVEIISRVHHRHLSVGYCI 339
Db 435 LLGSGGFGYVHKGVLPSGKEVAVKOLKVGSGQGEREFAVEIISRVHHRHLSVGYCI 494
QY 340 AGAKRLVYFVPPNNLHLHGEGRTPMWSSTRLKALGSAKLSYLEDNCPKTIHRD 399
Db 495 SENRLLIYDVPNNLHFLH--GTPGLDWARVKAAGARGLAYLHEDCPKTIHRD 552
QY 400 IKASNILIDFKFAKADFGAKTASDNTNTHSVTMGTGYLAPEYASGKLTESKDYF 459
Db 553 IKSSNILLNENFHALVDFG-LAKLDCNTHITTRVMGTFTGYMAPEYASGKLTESKDYF 612
QY 460 SFGVWLELITGRPDVANNVYDSDLVQWAPRLNASEQDFFGLADAKMNGYDREE 519
Db 613 SFGVWLELITGRPDVANNVYDSDLVQWAPRLNASEQDFFGLADAKMNGYDREE 672
QY 520 MARVACAAACVHRSAARRRPMQSIQVRALEGVNSLSDNEGMRPMQSIQVRALEGVNS 579
Db 673 MERMTAAACIRHSATKPRMSQIVRAFD-SLAEDLTNGMRGSEI-----IN 722
QY 580 SSQYNEWMKKFRKALGTQYIN 601
Db 723 SAQOQSAEIRLFRMAFGSQNYS 744

RESULT 7
F86369
hypothetical protein F508.10 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Dec-2001
C:Accession: F86369
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alor,
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Huizar, L.; Dewart, T.H.;
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719; PMID:11130712
A:Accession: F86369
A>Status: preliminary
A:Molecule type: DNA
```

A:Residues: 1-731 <STO>
 A:Cross-references: GB:AE005172; MID:g4056437; PIDN:AAC98010.1; GSPDB:GN00141
 C:Genetics:
 A:Map position: 1

Query Match 41.0%; Score 1415.5; DB 2; Length 731;
 Best Local Similarity 43.4%; Pred. No. 1.4e-38;
 Matches 321; Conservative 93; Mismatches 156; Indels 169; Gaps 22;

```

QY 2 SSAPSPGNGSPSPSSNTT-----TTPPAS-----APPTTSSPPP 40
  :|||:||||:||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 29 NSALPPVDSPPSPADSSSTPPEPTPPDPSQQLPPLPSILPLTDSPPSPSPV 88
  :|||:||||:||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 41 PSTIPTSPPSRSTSPAP-----PPSPPTSTPGSPPP-----LPQSPPA-----PTTP 86
  :|||:||||:||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 89 DST-PSPPPTSPSPSPSEPTPPAPPNESNDNNPPSQDLQSPSPSPSPVGNP 147
  :|||:||||:||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 87 GSPP-APVTPPTNP-----PPSVGPTSPN-----SREGSPSPSPSP-SPSPS----- 129
  :|||:||||:||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 148 ESPPLQSPAPPADPTNSPASPDLPTNPPIQPSGATSPAPNAPPSPPTVPPT 207
  :|||:||||:||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 130 -----SSDGLSTG-----VVVGIALGGVALLVITLIL 159
  :|||:||||:||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 208 PSSGPVYVPSLTSKGTPTNQNGDGGGGGFGQKTMVGMVAGFAIMALIGWFLV 267
  :|||:||||:||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 160 CKKRRDEEDAY-----YVPPP-----PPGPKAGGPGYGGQQOOWROONATP 202
  :|||:||||:||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 268 RRKKKR--NIDSYNHSYLPHPNFSVKSDGLYQDPCKGYSGGPNSGMYNNSOQOQSM 325
  :|||:||||:||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 203 PSDHVITSLP2PKAPSPPPPPPPPPMSSGGSDYSDRVLPPSPGLVLFKSKT 262
  :|||:||||:||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 326 GNSGTAG-----GGYPHQ-----MQSSGTPD-----SAILGSGQTH 358
  :|||:||||:||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 263 FTYDELRATNGFSEANLLGGGFGYVHKGLVPSGKEVAVKOLKVGSGGGEREQA 322
  :|||:||||:||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 359 FSYELAEITQGFARKNLLGGGFGCWKGLQGVYVAVKOLKAGSGGQDREFKA 418
  :|||:||||:||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 323 ISRVHRLVSLVGYCIAGAKRLVYEFVPPNNLLEHLHGEGRPTMEWSTRLKIALGSAK 382
  :|||:||||:||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 419 ISRVHRLVSLVGYCISDQRLVYEVSNQILLEHL-----EMSKVRVLAISAK 471
  :|||:||||:||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 363 GLSVLHEDCPKIIHROIKASNLILDKFPAK-----VADFLAKIA 424
  :|||:||||:||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 472 GLAYLHEDCPKIIHROIKASNLILDKFPAK-----VADFLAKIA 424
  :|||:||||:||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 425 SDANTHSTRVMTGFGYLAPEYASGKLTESKDVFSFGVLELITGRPVDAANNVYDD 484
  :|||:||||:||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 532 DTTQIRVSTRVMTGFGYLAPEYASGKLTESKDVFSFGVLELITGRPVDAANNVYDD 484
  :|||:||||:||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 485 SLVDWAPLLNRASEGDFGLADAKMNGYDREEMARVACAAVYRHSARRPRMSQI 544
  :|||:||||:||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 592 SLVEWAPLLNRASEGDFGLADAKMNGYDREEMARVACAAVYRHSARRPRMSQI 544
  :|||:||||:||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 545 VRALEGNVSLDLNEGMRPQSNVSYSGSTDYSDSQYNEDMKFKMALGTQENATG 604
  :|||:||||:||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 652 VRALEDGSDGLSNGIKTG-----STTYDSQYNEDMKFKMALGTQENATG 702
  :|||:||||:||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 605 EYSNPTSDGLYPSGSSSE 623
  :|||:||||:||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 703 LYS-----GNTSAKSSD 715
  :|||:||||:||||:|||||:|||||:|||||:|||||:|||||:|||||

```

RESULT 8

T04455
 hypothetical protein F4D11.90 - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C:Date: 30-Apr-1999 #sequence_revision 50-Apr-1999 #text_change 04-Mar-2000
 C:Accession: T04455
 R:Bevan, M.; Benes, V.; Rechmann, S.; Borkova, D.; Ansoorge, W.; Hoheisel, J.; Mewes, H.W.
 submitted to the Protein Sequence Database, April 1998
 A:Reference number: Z15360
 C:Accession: T04455
 A:Molecule type: DNA

A:Residues: 1-731 <BEV>
 A:Cross-references: EMBL:AL022537
 A:Experimental source: cultivar Columbia; BAC clone F4D11
 C:Genetics:

A:Map position: 4
 A:Introns: 326/1; 476/1; 505/1; 528/3; 557/2; 606/3; 660/3
 A:Note: F4D11.90
 C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase ho

Query Match 40.5%; Score 1399; DB 2; Length 731;
 Best Local Similarity 47.3%; Pred. No. 4.5e-38;
 Matches 317; Conservative 71; Mismatches 181; Indels 101; Gaps 19;

```

QY 1 MSASPSPTGSPSPS---PFSNSTTTTPPASAP-----PPTPSPPPPSTPIPTSPSPSSR 53
  :|||:||||:||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 114 LPAKPSPPSPSPSPSETVPPGN--TISPPRSLFSESTPPVNTASPPPS-----DPRRR 165
  :|||:||||:||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 54 S--TSPAPP---SPTPS--TPGSPPLPQSPAPPTTPGSPAPVITPPTNPPSPV- 105
  :|||:||||:||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 166 SGPKPSFPPIINSPPNPSPNTFSLPETSFPKPLSTTF--PSSSTPPPKSPAAVTL 223
  :|||:||||:||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 106 -----GPPSNPSREGSPSPSPSPSPSDGLST-----GVVV 140
  :|||:||||:||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 224 PFFGPAGQLDGTAVAPPICGVTEPKTSPAESISPTPQLVPKSLPVTTSYHSSAGFLF 263
  :|||:||||:||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 141 GIAIGVALLVITLILCLLCKKRR--DEEDAYVYPPPPPPGPKAGGPGYGGQQOOWROQ 198
  :|||:||||:||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 284 GGVIVGALLILGLLFLVEYRATRNNNSSAAHOSKTP-----SKVQHRGG 332
  :|||:||||:||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 139 NATPSSDHVITSLPPEKAPSPPPPPPPPPMSSSGSDYSDRVLPPSPGLVLF 258
  :|||:||||:||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 333 NAGTNQAHVIT--MPPPIHAK-----YISGGCDTKEN-----NSVAKNIM 372
  :|||:||||:||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 259 SKSTFTYELARATNGFSEANLLGGGFGYVHKGLVPSGKEVAVKOLKVGSGGGEREQA 318
  :|||:||||:||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 373 PSGMFSYEELSKATGFGSEENLGGGFGYVHKGLVPSGKEVAVKOLKVGSGGGEREQA 432
  :|||:||||:||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 319 EVEILSRVHRLVSLVGYCIAGAKRLVYEFVPPNNLLEHLHGEGRPTMEWSTRLKIAL 378
  :|||:||||:||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 433 EVDITISRVHRLVSLVGYCVNGDKRLVYEFVPPKDTLEFHLHENGSRGVSPEMEMRLIAV 492
  :|||:||||:||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 379 GSAGLSLHEDCPKIIHROIKASNLILDKFPAKVADEGLAKIATDNT---THVSTRV 435
  :|||:||||:||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 493 GAAGLAVLHEDCSTIIHROIKANILLDSFEAKVSDFGFLAKESDINSSTHISTRV 552
  :|||:||||:||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 436 MGTGTYLAPEYASGKLTESKDVFSFGVLELITGRPVDAANNVYDDSLVDWAPLLN 495
  :|||:||||:||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 553 VGIETNAPEYASGKLTESKDVFSFGVLELITGRPSITAKDSSTNOSLVWAPLLIT 612
  :|||:||||:||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 496 RASEQDPEGLADAKMNGYDREEMARVACAAVYRHSARRPRMSQIVRALEGNVSL 555
  :|||:||||:||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 613 KAISGESDFLVDRLKLNKNTDTQMANNAACACIROSALWRPMSQVVRALGEVALR 672
  :|||:||||:||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 556 DLNEGMRPQSNVSYSGSTDYSDSQYNEDMKFKMALGTQENATGYSNPTSDYGL 615
  :|||:||||:||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 673 KVEE---TGNSTVTSSENPNDI--TPRYGTNKRFF-----DFGSSDGYTSEGV 717
  :|||:||||:||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 616 YPSGSSSEGG 625
  :|||:||||:||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 718 NPSQSSEHQ 727
  :|||:||||:||||:|||||:|||||:|||||:|||||:|||||:|||||

```

RESULT 9

A95563
 probable protein kinase 60711-62822 [imported] - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
 C:Accession: A95563
 R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Aloni,
 Chn, C.F.; Chung, M.K.; Conn, L.; Conway, A.B.; Cressy, T.H.; Dewar,
 ansen, N.F.; Hughes, B.; Huizar, L.
 Nature 408, 816-820, 2000
 A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim.

Map position: 1

2 SSAPSGTGGSPPPSPNSTTTTPPPASA--pppTPSSpppppSTIPTSPppp

| | | | |
|----|-----|---|-----|
| Db | 577 | SILVEARPLLEIAEKGDISEWDPRLNDYVESEYVKMIETASCVHSAIKPRMVQV | 639 |
| QY | 545 | VRALEGVNSLSDNEGRPGQSNIYSYSGSTDYDSQYNEDMKFKRMA-----LGTQE | 599 |
| Db | 637 | WALDTRDRLSDLNGVKGQSRV-----YDSGQYNEIRIFRASESDSLGTN- | 686 |
| QY | 600 | YNATGEYSNPTSDY | 613 |
| Db | 687 | ---TCYY--PSDY | 695 |

ABSCYLL II
C96728
hypothetical protein F24J13.2 [imported] - Arabidopsis thaliana

[illegible]

A; Experimental source: cultivar Columbia
C; Genetics:
A; Gene: AtSP.F1707.1
A; Map position: 1
A; Introns: 136/1; 166/1; 189/3; 215/2; 264/3
C; Superfamily: kinase-related transforming protein; protein kinase homology

Query Match 28.2%; Score 973; DB 2; Length 321;
Best Local Similarity 61.7%; Pred. No. 7.1e-25;
Matches 192; Conservative 45; Mismatches 62; Indels 12; Gaps 3;

QY 242 SDAPVLPAPPGL---VLGFSKSTFTYEELARATNGFSEANLLGGQGFVVHKGVLPSKK 298
Db : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
13 ADSPSSPTAPSDVSAMVGSGQHFTYTEELEDTTEGSQNILGEGFGCVIKGLKDGR 72
QY 299 EVAVKQLKVGSGQGEREFOAEVEIISRVHRHLVSLGYCIAGAKRLLYTFEVNNLEL 358
Db : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
73 LVAVKQLKVGSGQDREFAEVEIISRVHRHLVSLGYCIADSERLLIYYENVQTLEH 132
QY 359 HLHGEGPTMEWSTRFLKIALGSKGLSYLHEDC-----NPKIIHRDIKASNILIDPFEA 413
Db : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
133 HLGKGPVLVWAKRVARIAVLPR----VVRICKTVSHPKIIHRDIKASNILDDDEFEE 188
QY 414 KVADFCLAKIASDNTNHVSRVMGTFGYLAPEAAASKLTEKSDVFSGVVLLFLITGR 473
Db : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
189 QVADFLGKLKNDTQTTHVSRVMGTFGYLAPEYAQSGLTDSDVTFSGVVLLELIIGRK 248
QY 474 PVCAANNVYDLSVDWARPLLNKASEOGDEGLADAKMNNGYDREEMARVACAAACVRH 533
Db : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
249 PVDNRNPGLGESLVGARPLKKAETGDFSELVDRELKHVKYKNVERMIETAAACVRY 308
QY 534 SARRRPRMSQI 544
Db : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
309 SGPKRPRMVGV 319

RESULT 13
T01502
probable serine/threonine-specific protein kinase (EC 2.7.1.-) T10M13.2 - Arabidopsis
C; Species: Arabidopsis thaliana (mouse-ear cress)
C; Date: 19-Feb-1999 #sequence_revision 19-Feb-1999 #text_change 04-Mar-2000
C; Accession: T01502
R; Johnson, A.F.; de la Bastide, M.; Lodhi, M.; Hoffman, J.; Hasegawa, A.; Gnoj, L.; Martienssen, R.; McCombie, W.
submitted to the EMBL Data Library, May 1997
A; Description: The sequence of the Arabidopsis thaliana T10M13 BAC.
A; Reference number: Z14346
A; Accession: T01502
A; Status: translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Residues: 1-707 <OH>
A; Cross-references: EMBL:AF001308; NID:g2104523; PID:g3912917
A; Experimental source: cultivar Columbia
C; Genetics:
A; Map position: 4S
A; Introns: 132/1; 256/1; 327/1; 451/1; 532/2; 581/3
A; Note: T10M13.2
C; Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homology
C; Keywords: phosphotransferase

Query Match 23.6%; Score 816.5; DB 2; Length 707;
Best Local Similarity 30.2%; Pred. No. 1.2e-19;
Matches 227; Conservative 94; Mismatches 191; Indels 239; Gaps 22;

QY 10 GSPPSP---PSNSTITT---PPASAPPTTPSPSPPPPTIPTSPSPSRSTPSAPPPSP 64
Db : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
27 GLPVSTLSPSTSPVITDLPAEPFRCHRYKFFAQQAEPQHSPPYSLSVADHPPISS 86
QY 65 TPSTGSPPLPDPS-----PPATTGSPPPAPVPPTRNPPPS----- 103
Db : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
87 HFSPKSMRNAQSPGAGLADAPAOSNGVLFDALTQPPLSPSISNCCKSDMKVLRKSIG 146
QY 104 -----VPGPPS----- 109

147 CHCVPIKLDILLNVSETPSNMNEAFATQGLPHQELINFVYLSLRNISMIDIT 206
 QY 110 -----NPREGG-----SPRPPSP-----SPRPPSP 129
 Db 207 PHSGISFASQASAINSLSHKIQSPITVGDYKLLNLTWFAAPAPQAPLVAASPHKA 266
 QY 130 SDGLSTG-----VVGIAIGGVALLVIVTEICLLCKKKRRRDEADAYYP 175
 Db 267 PSOGSSATTSVSPGKKRHPNLLIFSAAGVLLAILIIVL-VICSRALREE----- 317
 QY 176 PPPPGPKAGGPGVGGQQWQONATPPSDHVVTSLPPPKAPSPRPPPPPPPPFMS 235
 Db 318 -----KAPDPKRAVKPRNLDD-AGS 336
 QY 236 SGGSDYSDRPVLPPLPSGVLGFSKSTFYELARATNGFSANLIGQGFGVYVHKVLP 295
 Db 337 FGGG-----LPHEA-----STFCSYEELKEATSNFESASILGEGFGKYGILIA 382
 QY 296 SGKEVAVKOLKVGSGQGERFQAEVEILSRVHRLHLSLVGYCIA--GAKRLLVYEFVN 353
 Db 383 DGTAVAIAKLTSGGPGQKDFQVEIDMLSKLHRLNLVGLVYSSRDSSQHLLEYELVN 442
 QY 354 KMLEHLHGEGRP-----TMEWSTRLKIALGSAKGLSYLHEDCNPKLIHRDKASNILID 408
 Db 443 GSLEWNLG---PLGNCPLDWDTRKIALDARGLVYHEDSQSPVHHRDFKASNILLE 499
 QY 409 FKEAKVADFLAKIASD--TNFHVSTRVMGTGYLAPEYAAAGSKLTKESKDFSEFGVLE 467
 Db 500 NFNNAKVAADFGLAKQAPRGNHLSRVMGTGYVAPEYAMTGHLLVKSDDVSYGVVLE 559
 QY 468 LITGRPRDANNVYDSDVWARPLLNRASQGGFEGGLADAKMNGYDREEMARVACA 527
 Db 560 LITGRKPPVDMQSPSCQENLVITREVLN---DKDRLEELVDSRLGKYPKEDFIRVCTIA 616
 QY 528 AACVHRSARRPRMSQIV-----RALEGVYSLDNEGMRPQO-----SNV 568
 Db 617 AACVAPASQRMTGEVYQSLKMWORVVEYQDPVLN--SNKAPNRQSSATESEVTSSM 576
 QY 569 YSS--YGGSTDYD-----SSQYNEDMKKFR 591
 Db 677 FSSGPGYSLSAFDHENITRTVTFSEDLHEGR 707
 RESULT 14
 E84587
 Probable protein kinase [imported] - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C>Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 17-May-2002
 C:Accession: E84587
 R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
 euss, D.; Nierman, W.C.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.
 Nature 402, 761-768, 1999
 A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
 A:Reference number: A64420; MUID:20083487; PMID:10617197
 A:Accession: E84587
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-435 <STO>
 A:Cross-references: GB:AE002093; NID:g4512705; PIDN:AAD21758.1; GSPDB:GNO0139
 C:Genetics:
 A:Gene: At2g20300
 A:Map position: 2
 C:Superfamily: kinase-related transforming protein; protein kinase homology
 Query Match 23.2%; Score 802; DB 2; Length 435;
 Best Local Similarity 45.7%; Pred. No. 2.3e-19;
 Matches 182; Conservative 68; Mismatches 122; Indels 26; Gaps 9;
 QY 234 SSSGGSYSDRPVLPPLPSGVLGFSKSTFYELARATNGFSANLIGQGFGVYVHKV 293
 Db 3 SSSARSSGSDSLM----SSMATCALSVKTFILSELEKATDFSAKRLVIGSGFGRVYGS 58

294 LPSGKEVAVKOLKVGSGQGERFQAEVEILSRVHRLHLSLVGYCIAKAKLLVYEFVN 353
 Db 59 MEDGTEVAVKLLTDMQNRDEFIAVEMLSRHLRLVLLIGTIGRTRCLLYELVN 118
 QY 354 NNLEHLHGEGRPMTMWSITELKIALGSAKGLSYLHEDCNPKLIHRDKASNILIDFKEA 413
 Db 119 GSVEHLH-BG--TLDWDARLKIALGAARGLAYLHEDSNPVHHRDKASNVLEDDFT 175
 QY 414 KVADFGLAKIASDTNTHVSTRVMGTGYLAPEYAAAGSKLTKESKDFSEFGVYVHKV 473
 Db 176 KVSDFGLAREATEGSHSTRVMGTGYVAPEYAMTGHLLVKSDDVSYGVVLELLTGR 235
 QY 474 PVDANNVYDSDVWARPLLNRASQGGFEGGLADAKMNGYDREEMARVACAACVVRH 533
 Db 236 PVDMSQPSGSENLVYWARPLL--ANREG-LEQLVDPALACTYNFDDMAKVAALASMCVHQ 292
 QY 534 SARRRPRMQQIVRALEGNVSLDNEGMRPQSNVYSSYGGSTDY-----DSSQYN-- 584
 Db 293 EVSHRPFMGVQALK--LIYNDADETCGYCQKQSDVPSADFKGLDAPSSDSSWNLT 350
 QY 585 EDMKTRKALGTQFYNATGEYSNPDSYGLYPSGSS 622
 Db 351 PRLRYGQASSFTPMDSY-----SGPLEDMENRPHSASS 383
 RESULT 15
 G96593
 Probable protein kinase, 86372-89112 [imported] - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C>Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
 C:Accession: G96593
 R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, M.A.; Kaul, S.; White, O.; Alci-
 Chan, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar,
 ansen, N.F.; Hughes, B.; Ruizar, L.
 Nature 408, 816-820, 2000
 A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim
 C.A.; Li, J.H.; Li, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marzi
 Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
 A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tall-
 ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
 A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
 A:Reference number: A86141; MUID:21016719; PMID:11130712
 A:Accession: G96593
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-676 <STO>
 A:Cross-references: GB:AE005173; NID:g10645416; PIDN:AAG21533.2; GSPDB:GNO0141
 C:Genetics:
 A:Gene: F7A10.8
 A:Map position: 1
 Query Match 22.4%; Score 774; DB 2; Length 676;
 Best Local Similarity 48.6%; Pred. No. 2.6e-18;
 Matches 156; Conservative 57; Mismatches 94; Indels 14; Gaps 3;
 QY 248 PPPSPGL-----VLGFSKSTFYELARATNGFSANLIGQGFGVYVHKVPSCK 298
 Db 343 PPVSPCLSCIOHKAPVFGKPPRFYSYKELELATNGFSANLAEGGFSVHGVLPQEQ 402
 QY 299 EVAVKOLKVGSGQGERFQAEVEILSRVHRLHLSLVGYCIAKAKLLVYEFVNKNLE 358
 Db 403 IVAVKOHKVASQTQGDVEFCSEVLSCAQHNRVVMVLIIGFCIEDTRLLVYETICNGSLDS 462
 QY 359 HLHGEGRPMTMWSITELKIALGSAKGLSYLHEDCNPK--IHRDKASNILIDFKEAKVAD 417
 Db 463 HLYGRKDTLGPAPAKITAVGAARGRLVHRCRVCIVHRRNPNILETHDYELPVD 522
 QY 418 FGLAKIASDTNTHVSTRVMGTGYLAPEYAAAGSKLTKESKDFSEFGVYVHKV 477
 Db 523 FGLARQPDGLGVDTRTVIGTGYLAPEYAGQITEKADVYSFGVWLELITGRKADI 582
 QY 476 NNVYDSDVWARPLLNRASQGGFEGGLADAKMNGYDREEMARVACAACVVRHARR 537

Db 583 YRPKGCCTEWARSL---EYAVEELVDPLEKRYSETQVICMHTASLCIRRDPHL 638
QY 538 RPRMSQIVRALEGNVSLDLN 558
Db 639 RPRMSQVLRLEGEMLMNEIS 659

Search completed: July 2, 2003, 13:25:21
Job time : 56 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 2, 2003, 15:19:04 ; Search time 88 Seconds
(without alignments)
1514.915 Million cell updates/sec

Title: US-10-086-464-2
Perfect score: 3453
Sequence: 1 MSSAPSGTGGPPSPNSST.....REMEMGKIKRTGGYSGPSL 647

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: SP_TREMBL_21.*
- 2: sp_archaea.*
- 3: sp_bacteria.*
- 4: sp_fungi.*
- 5: sp_human.*
- 6: sp_invertebrate.*
- 7: sp_mammal.*
- 8: sp_mmc.*
- 9: sp_organelle.*
- 10: sp_phase.*
- 11: sp_plant.*
- 12: sp_ricent.*
- 13: sp_virus.*
- 14: sp_vertebrate.*
- 15: sp_unclassified.*
- 16: sp_rvirus.*
- 17: sp_bacteriap.*
- 17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB | ID | Description |
|------------|--------|-------------|--------|----|--------|--------------------|
| 1 | 3453 | 100.0 | 647 | 10 | Q9ARH1 | Q9arhl brassica na |
| 2 | 2936.5 | 85.0 | 652 | 10 | Q9LV48 | Q9lv48 arabidopsis |
| 3 | 2934.5 | 85.0 | 652 | 10 | Q94JZ6 | Q94jz6 arabidopsis |
| 4 | 1821.5 | 52.8 | 597 | 10 | Q8W0B8 | Q8w0b8 oryza sativ |
| 5 | 1769 | 51.2 | 458 | 10 | Q9LX03 | Q9lx03 arabidopsis |
| 6 | 1748.5 | 50.6 | 633 | 10 | Q9ZK08 | Q9zkg8 arabidopsis |
| 7 | 1729 | 50.1 | 699 | 10 | Q9X196 | Q9xi96 arabidopsis |
| 8 | 1687 | 48.9 | 674 | 10 | Q65672 | Q65672 arabidopsis |
| 9 | 1656.5 | 48.0 | 714 | 10 | Q9LS95 | Q9ls95 arabidopsis |
| 10 | 1513.5 | 43.8 | 710 | 10 | Q9CAL8 | Q9cal8 arabidopsis |
| 11 | 1459.5 | 42.3 | 708 | 10 | Q9LV50 | Q9lv50 arabidopsis |
| 12 | 1459.5 | 42.3 | 708 | 10 | Q9SX31 | Q9sx31 arabidopsis |
| 13 | 1456 | 42.2 | 681 | 10 | Q9FTW5 | Q9ffw5 arabidopsis |
| 14 | 1434 | 41.5 | 760 | 10 | Q9C660 | Q9c660 arabidopsis |
| 15 | 1415.5 | 41.0 | 731 | 10 | Q9ZUE0 | Q9zue0 arabidopsis |
| 16 | 1399 | 40.5 | 731 | 10 | Q65530 | Q65530 arabidopsis |

| | | | | | | |
|----|--------|------|------|----|--------|--------------------|
| 17 | 1397 | 40.5 | 509 | 10 | Q9C821 | Q9c821 arabidopsis |
| 18 | 1396 | 40.4 | 698 | 10 | Q9ASK4 | Q9ask4 oryza sativ |
| 19 | 1322.5 | 40.3 | 568 | 10 | Q9AY15 | Q9ay15 oryza sativ |
| 20 | 1233 | 35.7 | 715 | 10 | Q9SGY7 | Q9sgy7 arabidopsis |
| 21 | 1222.5 | 35.4 | 610 | 10 | Q943G8 | Q943g8 oryza sativ |
| 22 | 1215 | 35.2 | 752 | 10 | Q9LQC5 | Q9lqc5 arabidopsis |
| 23 | 1209.5 | 35.0 | 501 | 10 | Q9AYA6 | Q9aya6 oryza sativ |
| 24 | 1103 | 31.9 | 628 | 10 | Q9ATJ7 | Q9atj7 oryza sativ |
| 25 | 1022 | 29.6 | 394 | 10 | Q9CAL9 | Q9cal9 arabidopsis |
| 26 | 993 | 28.8 | 378 | 10 | Q9FW38 | Q9fw38 oryza sativ |
| 27 | 973 | 28.2 | 321 | 10 | Q64591 | Q64591 arabidopsis |
| 28 | 927 | 26.8 | 1111 | 10 | Q9FH74 | Q9fh74 arabidopsis |
| 29 | 921.5 | 26.7 | 1014 | 10 | Q9FT38 | Q9ft38 oryza sativ |
| 30 | 840 | 24.3 | 744 | 10 | Q8FWQ0 | Q8fwq0 arabidopsis |
| 31 | 839 | 24.3 | 794 | 10 | Q9ASFQ | Q9asf0 oryza sativ |
| 32 | 828.5 | 24.0 | 820 | 10 | Q9SNF3 | Q9snf3 oryza sativ |
| 33 | 816.5 | 23.6 | 707 | 10 | Q04245 | Q04245 arabidopsis |
| 34 | 802 | 23.2 | 435 | 10 | Q9SK72 | Q9sk72 arabidopsis |
| 35 | 791.5 | 22.9 | 753 | 10 | Q9LTC9 | Q9ltc9 arabidopsis |
| 36 | 788.5 | 22.8 | 748 | 10 | Q8W0N1 | Q8w0n1 oryza sativ |
| 37 | 787.5 | 22.8 | 479 | 10 | Q94KD9 | Q94kd9 arabidopsis |
| 38 | 780.5 | 22.6 | 472 | 10 | Q23699 | Q23699 arabidopsis |
| 39 | 776.5 | 22.5 | 669 | 10 | Q93ZU1 | Q93zu1 arabidopsis |
| 40 | 774 | 22.4 | 676 | 10 | Q9C890 | Q9c890 arabidopsis |
| 41 | 773 | 22.4 | 492 | 10 | Q22764 | Q22764 arabidopsis |
| 42 | 769.5 | 22.3 | 450 | 10 | Q04601 | Q04601 arabidopsis |
| 43 | 766 | 22.2 | 516 | 10 | Q9AWQ0 | Q9awq0 oryza sativ |
| 44 | 764 | 22.1 | 497 | 10 | Q9LMM7 | Q9lmm7 arabidopsis |
| 45 | 757 | 21.9 | 523 | 10 | Q9SZC0 | Q9szc0 arabidopsis |

ALIGNMENTS

RESULT 1

Q9ARH1 PRELIMINARY; PRT; 647 AA.

AC Q9ARH1; AT Q1-JUN-2001 (TREMBLrel. 17, Created)

DT Q1-JUN-2001 (TREMBLrel. 17, Last sequence update)

DT Q1-MAR-2002 (TREMBLrel. 20, Last annotation update)

DE Receptor protein kinase PERK1.

OS Brassica napus (Rape).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Brassica.

OX NCBI_taxid=3708;

RN [1]

RP SEQUENCE FROM N.A.

RA Silva N.F., Goring D.R.;

RT "Characterization of a novel Brassica napus receptor protein kinase PERK1."

RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.

CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.

DR EMBL; AY028699; AAK21965.1; -

DR InterPro; IPR000719; Euk_pkinase.

DR InterPro; IPR002965; P_rich_extensn.

DR InterPro; IPR002290; Ser_thr_pkinase.

DR Pfam; PF00069; pkinase; 1.

DR PRINTS; PR01217; PRICHTEXTENS.

DR PRINTS; PR00109; TYRKINASE.

DR ProDom; PD000001; Euk_pkinase; 1.

DR SMART; SM00220; S_TKC; 1.

DR SMART; SM00219; Tyrc; 1.

DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.

DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.

DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.

KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.

SQ SEQUENCE 647 AA; 68482 MW; A69AEAC0D5CA203 CRC64;

Query Match 100.0%; Score 3453; DB 10; Length 647;
Best Local Similarity 100.0%; Pred. No. 6.4e-216;

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Matches 647; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MSSAPSGTGGSPSPSSNSTTTTPPPASAPPTTPSSPPPTTPTSPSPSSRSSESAPP 60
DB 1 MSSAPSGTGGSPSPSSNSTTTTPPPASAPPTTSSPPPTTPTSPSPSSRSSESAPP 60
QY 61 FSPPTPTGSPSPSPSPSPSPSPSPSPSPSPSPSPSPSPSPSPSPSPSPSPSPSPSP 120
DB 61 FSPPTPTGSPSPSPSPSPSPSPSPSPSPSPSPSPSPSPSPSPSPSPSPSPSPSPSP 120
QY 121 PSSPSPSPSPSPSPSPSPSPSPSPSPSPSPSPSPSPSPSPSPSPSPSPSPSPSP 180
DB 121 PSSPSPSPSPSPSPSPSPSPSPSPSPSPSPSPSPSPSPSPSPSPSPSPSPSPSP 180
QY 181 GPKAGPYGGGQQQARQONATPPSDHVTSLPPPKAPSPRQPPPPPPPPPMSSSGSD 240
DB 181 GPKAGPYGGGQQQARQONATPPSDHVTSLPPPKAPSPRQPPPPPPPPPMSSSGSD 240
QY 241 YSDRVLPPSPGLVGLFSKSTFTYEELARATNGFSEANLLGQGGFGYVHKGLVPSGKEV 300
DB 241 YSDRVLPPSPGLVGLFSKSTFTYEELARATNGFSEANLLGQGGFGYVHKGLVPSGKEV 300
QY 301 AVKQLKVGSGGGERFQAEVELISRVHRHLVSLNGYCIAGAKRLVLYEFPNNLELHL 360
DB 301 AVKQLKVGSGGGERFQAEVELISRVHRHLVSLNGYCIAGAKRLVLYEFPNNLELHL 360
QY 361 HGEGRPTMEWTRLKIALGSAKLSYLHEDCNPKIIHRDIKASNLILDFKFEAKVADFL 420
DB 361 HGEGRPTMEWTRLKIALGSAKLSYLHEDCNPKIIHRDIKASNLILDFKFEAKVADFL 420
QY 421 AKIASDNTHTVTRVMGTFGLAEPYASGKLTFSKVSFGVVLLELITGRPPVDANNV 480
DB 421 AKIASDNTHTVTRVMGTFGLAEPYASGKLTFSKVSFGVVLLELITGRPPVDANNV 480
QY 481 YVDSLVDWARPLNLRASEQDFFGLADAKNNNGYDREEMRVACAAACVHRHSARRRPR 540
DB 481 YVDSLVDWARPLNLRASEQDFFGLADAKNNNGYDREEMRVACAAACVHRHSARRRPR 540
QY 541 MSQIVRALEGNVSLSDNEGMRPQGSNNYSSYGSTVDYSDQYEDMDKFKRMALGTQY 600
DB 541 MSQIVRALEGNVSLSDNEGMRPQGSNNYSSYGSTVDYSDQYEDMDKFKRMALGTQY 600
QY 601 NATGEYSNPTSDYGLTSGSSSEGGTTREMEMGKIKRTGQYSGPSL 647
DB 601 NATGEYSNPTSDYGLTSGSSSEGGTTREMEMGKIKRTGQYSGPSL 647

RESULT 2
Q9LV48 PRELIMINARY; PRT; 652 AA.
AC Q9LV48:
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DE 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Protein Kinase-like protein (AT3g24550/MOB24_8) (Hypothetical 59.3 kDa protein).
DE NCBI_TaxID=3702;
GN MOB24_13 OR AT3G24550.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliopsida; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=COLOMBIA;
RA Kaneko I., Sato T., Nakamura Y., Asamizu E., Tabata S.;
RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=COLOMBIA;
RX MEDLINE=20363099; PubMed=10907853;
RA Nakamura Y.;
RT *Structural analysis of Arabidopsis thaliana chromosome 3. II.

```

```

RT Sequence features of the regions of 4,251,695 bp covered by ninety P1,
RT TAC and BAC clones.;
RL DNA Res. 7:217-221(2000).
RN [3]
RP SEQUENCE FROM N.A.
RA Nguyen M., Karlin-Neumann G., Southwick A., Lam B., Miranda M.,
RA Palm C.J., Bowser L., Jones T., Banh J., Carninci P., Chen H.,
RA Cheuk R., Chung M.K., Hayashizaki Y., Ishida J., Kamiya A., Kawai J.,
RA Kim C., Lin J., Liu S.X., Narusaka M., Pham P.K., Sakano H.,
RA Sakurai T., Satou M., Seki M., Shinn P., Yamada K., Shinozaki K.,
RA Ecker J., Theologis A., Davis R.W.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RA Cheuk R., Chen H., Kim C.J., Koesema E., Meyers M.C., Banh J.,
RA Bowser L., Carninci P., Dale J.M., Goldsmith A.D., Hayashizaki Y.,
RA Ishida J., Jiang P.X., Jones T., Kamiya A., Karlin-Neumann G.,
RA Kawai J., Lam B., Lee J.M., Lin J., Liu S.X., Miranda M., Narusaka M.,
RA Nguyen M., Onodera C.S., Palm C.J., Pham P.K., Quach H.L., Sakurai T.,
RA Satou M., Seki M., Southwick A., Tang C.C., Toriumi M., Yamada K.,
RA Yamamura Y., Yu G., Yu S., Shinozaki K., Davis R.W., Theologis A.,
RA Ecker J.R.;
RL Arabidopsis cDNA clones.;
RT Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RA Southwick A., Karlin-Neumann G., Nguyen M., Lam B., Miranda M.,
RA Palm C.J., Bowser L., Jones T., Banh J., Carninci P., Chen H.,
RA Cheuk R., Chung M.K., Hayashizaki Y., Ishida J., Kamiya A., Kawai J.,
RA Kim C., Lin J., Liu S.X., Narusaka M., Pham P.K., Sakano H.,
RA Sakurai T., Satou M., Seki M., Shinn P., Yamada K., Shinozaki K.,
RA Ecker J., Theologis A., Davis R.W.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL; AB020746; BAB02007.1; -
DR EMBL; AY059901; AAL24383.1; -
DR EMBL; AY056788; AAL10479.1; -
DR EMBL; AY093065; AAM13064.1; -
DR InterPro; IPR000719; Euk_pkinase.
DR InterPro; IPR002965; P-rich_extensn.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR InterPro; IPR004040; Ser_thr_pkinase.
DR InterPro; IPR001245; Tyr_pkinase.
DR Pfam; PF00069; pkinase; 1.
DR PRINTS; PRO1217; PRICHEXTENS.
DR PROSITE; PS0109; TYRKINASE.
DR ProDom; PD000001; Euk_pkinase; 1.
DR SMART; SM00221; STYK; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW Hypothetical protein; ATP-binding; Kinase;
KW Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 652 AA; 69271 MW; 35005EE29FE8602F CRC64;

Query Match 85.0%; Score 2936.5; DB 10; Length 652;
Best Local Similarity 87.0%; Pred. No. 2.1e-182;
Matches 574; Conservative 24; Mismatches 41; Indels 21; Gaps 12;
QY 1 MSSAPSGT---GSPSPSPSSNTTTTPPPA--SAPPPTTPSPPP--PSTIPTSPSPSSRS 54
DB 1 MSTAPSGTTPSPSPSPSPSTTTTPPPAASSPPPTTTPSPSPSPSTNSTSPSPSPSPL 60
QY 55 TPSAPPTTPPTTPSPSPSPPTTPPPAAPTTPPTTPPTTPPTTPPTTPPTTPPTTPPTTP 113
DB 61 PPSLPPTSPSPGSLT----PPLPQSPSPAPITP--GPPSTTPSPSPSPSPGPPPTSPS- 114
QY 114 EGSPSPSPSS--PSPSPSPSDGLSTGVVGAIGVALLVITVLICLCKKRRR--DEE 169
DB 115 -GSTPRTPTNTKPSPPSPSDGLSTGVVGAIGVALLVITVLICLCKKRRRHDE 173
QY 170 DAYTVPPPPPPGPKAGPYGGQQQARQONATPPSD-HVVTSLPPPPKAPSPRQPPPP 229
DB 170 DAYTVPPPPPPGPKAGPYGGQQQARQONATPPSD-HVVTSLPPPPKAPSPRQPPPP 229

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Db 174 AAYVPPPPSPGKAGGPGYGGQQYVWQQNARPSNDNHVVTSL--PPPKPSPPPKPPPPPP 232
QY 229 PPP-FMSSSGSDYSDRPLVPPSPGLWIGFSGKSTFTYEELARATNGFSEANLLGGQGGF 287
Db 233 PPAPFSSSGSDYSDLPVPPSPGLWIGFSGKSTFTYEELSRATNGFSEANLLGGQGGF 292
QY 288 YVHGVLPSGKEAVAKQLKVGSGQGEREFOAEVEIISRVHRLHLSLVGFCIAGAKRLV 347
Db 293 YVHGILPSGKEAVAKQLKAGSGQGEREFOAEVEIISRVHRLHLSLVGFCMAGVQRLV 352
QY 348 YEEVPPNNLEHLHGEGRPTMEWSTRLKIALGSAKGLSYLHEDCNPKIIHRDIKASNLI 407
Db 353 YEEVPPNNLEHLHGEGRPTMEWSTRLKIALGSAKGLSYLHEDCNPKIIHRDIKASNLI 412
QY 408 DFEAKVADFGGLAKIASDTNTHVSTVWMTGTFGLAPEYAAAGKLTSEKSDVSEFGVLL 467
Db 413 DFEAKVADFGGLAKIASDTNTHVSTVWMTGTFGLAPEYAAAGKLTSEKSDVSEFGVLL 472
QY 468 LITGRPPVDANNVYDDSLVDWAPRLNRASEGDFGLADAKMNGYDREEMARWACA 527
Db 473 LITGRPPVDANNVYDDSLVDWAPRLNRASEGDFGLADAKMNGYDREEMARWACA 532
QY 528 AACVRSARRPRMSQIVRALEGNVSLDNEGMRPGQSNVYSSGSDYDSSQYNDM 587
Db 533 AACVRSARRPRMSQIVRALEGNVSLDNEGMRPGHSHNVYSSGSDYDTSQYNDM 592
QY 588 KFERKMGALGTQENATGEYSNPTSDYGLYPSGSSSEGTTRMEMGKIKRTGGYSGPSL 647
Db 593 IKFERKMGALGTQEGTGEYSNPTSDYGLYPSGSSSEGTTRMEMGKIKRTGGYSGPSL 652

RESULT 3
Q94JZ6 PRELIMINARY; PRT; 652 AA.
ID Q94JZ6 AC Q94JZ6
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-MAR-2002 (TrEMBLrel. 19, Last sequence update)
DE 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Putative kinase-like protein.
GN MOB24.13.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Southwick A., Karlin-Neumann G., Nguyen M., Lam B., Miranda M.,
RA Palm C.J., Bowser L., Jones T., Banh J., Carninci P., Chen H.,
RA Cheuk R., Chung M.K., Hayashizaki Y., Ishida J., Kamiya A., Kawai J.,
RA Kim C., Lin J., Liu S.X., Narusaka M., Pham P.K., Sakano H.,
RA Sakurai T., Satou M., Seki M., Shinn P., Yamada K., Shinozaki K.,
RA Ecker J., Theologis A., Davis R.W.
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF370509; AAK43866.1; -.
DR InterPro: IPR000719; Euk_pkinase.
DR Pfam: PF00069; pkinase; 1.
DR ProDom: PD000001; Euk_pkinase; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; UNKNOWN_1.
DR PROSITE: PS00111; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS01008; PROTEIN_KINASE_ST; UNKNOWN_1.
KW ATP-binding; Kinase; Transferase.
SQ SEQUENCE 652 AA; 69271 MW; F2530AE5CCBD102E CRC64;

Query Match 85.0%; Score 2934.5; DB 10; Length 652;
Best Local Similarity 86.8%; Pred. No. 2.8e182;
Matches 573; Conservative 25; Mismatches 41; Indels 21; Gaps 12;

QY 1 MSSAPSPGPT--GSPSPSPSNSTTTTPPA--SAPPTTPSPPP--PSTIPTSPSPSSRS 54
Db 1 MSTAPSPGTPSPSPPTNSTTTTPPAASPPPTTTPSPSPSPSTNSTISPPSPSPL 60

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QY 55 TPSAPPPSPPTSPGSPPLPQPSPPTTPGSPAPVPTPT--RNPPSPVSPGSPSPNSR 113
Db 51 PPSLPPSPSPSLT----PPIQPSAPITP--SPSPTTPSNRSPSPNOGPNTPS- 114
QY 114 EGSPPRPSS--PSPSPSSDGLSTGVVGAIGVALLVITLCLCKKKRR--DEE 169
Db 115 -GSTPRTSNKPSPPSDSGLSTGVVGAIGVAILVITLCLCKKKRRRHDE 173
QY 170 DAYVPPPPPPGKAGGPGYGGQQQWRCQNTPPSD--HVVTSLPPPKAPSPRPPPP 228
Db 174 AAYVPPPPPPGKAGGPGYGGQQQWRCQNTPPSD--HVVTSLPPPKAPSPRPPPP 232
QY 229 PPP-FMSSSGSDYSDRPLVPPSPGLWIGFSGKSTFTYEELARATNGFSEANLLGGQGGF 287
Db 233 PPAPFSSSGSDYSDLPVPPSPGLWIGFSGKSTFTYEELSRATNGFSEANLLGGQGGF 292
QY 288 YVHGVLPSGKEAVAKQLKVGSGQGEREFOAEVEIISRVHRLHLSLVGFCIAGAKRLV 347
Db 293 YVHGILPSGKEAVAKQLKAGSGQGEREFOAEVEIISRVHRLHLSLVGFCMAGVQRLV 352
QY 348 YEEVPPNNLEHLHGEGRPTMEWSTRLKIALGSAKGLSYLHEDCNPKIIHRDIKASNLI 407
Db 353 YEEVPPNNLEHLHGEGRPTMEWSTRLKIALGSAKGLSYLHEDCNPKIIHRDIKASNLI 412
QY 408 DFEAKVADFGGLAKIASDTNTHVSTVWMTGTFGLAPEYAAAGKLTSEKSDVSEFGVLL 467
Db 413 DFEAKVADFGGLAKIASDTNTHVSTVWMTGTFGLAPEYAAAGKLTSEKSDVSEFGVLL 472
QY 468 LITGRPPVDANNVYDDSLVDWAPRLNRASEGDFGLADAKMNGYDREEMARWACA 527
Db 473 LITGRPPVDANNVYDDSLVDWAPRLNRASEGDFGLADAKMNGYDREEMARWACA 532
QY 528 AACVRSARRPRMSQIVRALEGNVSLDNEGMRPGQSNVYSSGSDYDSSQYNDM 587
Db 533 AACVRSARRPRMSQIVRALEGNVSLDNEGMRPGHSHNVYSSGSDYDTSQYNDM 592
QY 588 KFERKMGALGTQENATGEYSNPTSDYGLYPSGSSSEGTTRMEMGKIKRTGGYSGPSL 647
Db 593 IKFERKMGALGTQEGTGEYSNPTSDYGLYPSGSSSEGTTRMEMGKIKRTGGYSGPSL 652

RESULT 4
Q8W0B8 PRELIMINARY; PRT; 597 AA.
ID Q8W0B8 AC Q8W0B8
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DE 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Putative receptor protein kinase PERK1.
GN P0452F10.5.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzeae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-CV. NIPPONBARE;
RA Sasaki T., Matsumoto T., Yamamoto K.;
RT "Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC
RT clone:P0452F10.";
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AP003434; BAB78668.1; -.
DR InterPro: IPR000719; Euk_pkinase.
DR InterPro: IPR000847; HTH_LysR.
DR InterPro: IPR002290; Ser_thr_pkinase.
DR InterPro: IPR001245; Tyr_pkinase.
DR Pfam: PF00069; pkinase; 1.
DR ProDom: PD000001; Euk_pkinase; 1.
DR SMART: SM00220; S_TKC; 1.
DR SMART: SM00219; TYKC; 1.
DR PROSITE: PS00044; HTH_LYSR_FAMILY; UNKNOWN_1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; UNKNOWN_1.

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|-----------------------|--|
| OC | eurosid II; Brassicales; Brassicaceae; Arabidopsis. |
| OX | NCBI_TaxID=3702; |
| RN | [1] |
| RP | SEQUENCE FROM N.A. |
| RC | STRAIN-CV. COLUMBIA; |
| RX | MEDLINE-20083487; PubMed-10617197; |
| RA | Liu X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D., Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldhlyum T.V., Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H., Moffat K.S., Cronin L.A., Shen M., VanAken S.E., Unmayam L., Tallon L.J., Gill J.E., Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R., Copenhaver G.P., Preuss D., Nietman W.C., White O., Eisen J.A., Salzberg S.L., Fraser C.M., Venter J.C.; |
| RA | "Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana"; |
| RT | Nature 402:761-768(1999). |
| RN | [2] |
| RP | SEQUENCE FROM N.A. |
| RC | STRAIN-CV. COLUMBIA; |
| RA | Liu X., |
| RN | Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases. |
| RP | [3] |
| RC | SEQUENCE FROM N.A. |
| RA | STRAIN-CV. COLUMBIA; |
| RX | Liu X., Kaul S., Shea T.P., Fujii C.Y., Shen M., VanAken S.E., Barnstead M.E., Mason T.M., Bowman C.L., Ronning C.M., Benito M.-I., Carrera A.J., Creasy T.H., Buell C.R., Town C.D., Mierman W.C., Fraser C.M., Venter J.C.; |
| RA | Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases. |
| CC | -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES. |
| DR | EMBL; ACC06135; AAM12219.1; -; |
| DR | EMBL; ACC06439; AAM15257.1; -; |
| DR | InterPro; IPR000719; Euk.pkinase. |
| DR | InterPro; IPR002965; P-rich.extensn. |
| DR | InterPro; IPR002290; Ser.thr.pkinase. |
| DR | InterPro; IPR004040; STY.pkinase. |
| DR | Pfam; PF00069; pkinase; 1. |
| DR | PRINTS; PR01217; PRICHEXTENS. |
| DR | ProDom; PD000001; Euk.pkinase; 1. |
| DR | SMART; SM00221; STYK; 1. |
| DR | PROSITE; PS00107; PROTEIN_KINASE_ATP; 1. |
| DR | PROSITE; PS00011; PROTEIN_KINASE_DOM; 1. |
| DR | PROSITE; PS00108; PROTEIN_KINASE_ST; 1. |
| KW | Hypothetical protein; ATP-binding; Serine/threonine-protein kinase; Transferase. |
| KW | TRANSFERASE |
| SQ | SEQUENCE 633 AA; AF92060E5493C845 CRC64; |
| Query Match | 50.6%; Score 1748.5; DB 10; Length 633; |
| Best Local Similarity | 56.8%; Pred. No. 2.3e-135; |
| Matches | 363; Conservative 78; Mismatches 151; Indels 47; Gaps 15; |
| QY | 3 SAPSPCTGPPPPSSNSTTTTPPASAPPTTFSSPPPTTPTSPPSRSSTPSAPPSP 62 : : : : : : : : |
| Db | 7 SAPPTNSTSPSPSNNTSTTSF---PAPSFPPTPGQDSSSPPTSTSPAPCAPN 63 : : : : : : : : |
| QY | 63 PTPPTGGPPPLPQPSPAPTTPGSPAPVPATPTRNPPSPVPSPNSREGGSER--P 120 : : : : : : : : : : |
| Db | 64 PPN-SNNSPSPSGGGGRGNNGNDTPSRGSPPS---PPSRSGNDNGSKRSSP 119 : : : : : : : : : : |
| QY | 121 PS-----SPSPSP--SSDG-----LSTGVVVGIAAGVALLVICLLCKKKR 165 : : : : : : : : |
| Db | 120 PGDTGSRSDNPSPSGSGSGGGGGGGRGNTNTAIIVGLVGAGLITVLIVLRKKKR 179 : : : : : : : : |
| QY | 166 RDEDAAYVPPPPPPPKAGGP--XGGQQQOQRQONATPPSDHVVTLSPPPPAPSPPR 222 : : : : : : : : |
| Db | 180 ----DSFY-----PEPMKGNQYYIGNNNNASQY--PNHLNMQSQNQOSTGWGG 227 : : : : : : : : |
| QY | 223 QPPPPPPPFMSGG--GDYS--DRPVLPSPGLVGFSGKSTFTYEELARATINGFSEA 278 : : : : : : : : |
| Db | 228 GGSPPPPPRMPTSGEDSMYSGSPRLVPPSPALALGNKSTFTTYQLAAATGFTDA 287 : : : : : : : : |
| QY | 279 NLQGCGGFGVGHKVLPSGKEVAVKLSKAGSGGGEREQAEVDIIISRVHHRLVSLVGYC 338 : : : : : : : : |
| Db | 288 NLQGCGGFGVGHKVLPSGKEVAVKLSKAGSGGGEREQAEVDIIISRVHHRLVSLVGYC 347 |
| QY | 339 IAGAKRLLVYEFVNPNNELEHLHGEGRTMEWETRLKIALGSAKGLSYLHEDCNPKTIHR 398 : : : : : : : : |
| Db | 348 IADGQRLVYEFVNPKTLEVHLHGKNLPYMEFSTRLEIALGAAGLAYLHEDCHPRIHR 407 : : : : : : : : |
| QY | 399 DIKASNILIDKFKEAVADVADGLAKIASDTNTHSVTRVMGTFGYLAFYAASGKLITEKSOV 458 : : : : : : : : |
| Db | 408 DIKASNILDFDNADVADGLAKIASDTNTHSVTRVMGTFGYLAFYAASGKLITEKSDV 467 : : : : : : : : |
| QY | 459 FSGGVVLELITGRRPVDANNVYDDSLVDWARPLNRASEQDFESGLADAKNMNGYDRE 518 : : : : : : : : |
| Db | 468 FSYGMVLELITGKRPVD-NSITMDTLDYDMARLMARALEGNENELADLEGNYNPQ 526 : : : : : : : : |
| QY | 519 EMARMVACAAACVRHSARRRRPRMSQIVRALGNSVSLDLNEGMRPGSGNSYISTGGSTDY 578 : : : : : : : : |
| Db | 527 EMARMVTCAASTPHSGRKPKMSQIVRALEGEVSILDALNEGVKPGHSGHYSGIGASSDY 586 : : : : : : : : |
| QY | 579 DSSQYNEDMKFRMALTQIEY---NATGEYSNPTSDYG 614 : : : : : : : : |
| Db | 587 SQTSYNADMKKFQRIALSQEPFVDCSEGSTSSNDSRDWG 625 |
| RESULT 7 | |
| Q9XI96 | PRELIMINARY; PRT; 699 AA. |
| AC | O9XI96; |
| ID | O1-NOV-1999 (TrEMBLrel. 12, Created) |
| DT | O1-NOV-1999 (TrEMBLrel. 12, Last sequence update) |
| DT | O1-MAR-2002 (TrEMBLrel. 20, Last annotation update) |
| DE | Similar to somatic embryogenesis receptor-like kinase. |
| GN | F13F21.28. |
| OS | Arabidopsis thaliana (Mouse-ear cross). |
| OC | Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; |
| OC | Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; |
| OC | eurosid II; Brassicales; Brassicaceae; Arabidopsis. |
| OX | NCBI_TaxID=3702; |
| RN | [1] |
| RP | SEQUENCE FROM N.A. |
| RA | Federspiel N.A., Palm C.J., Conway A.B., Conn L., Hansen N.F., Altafi H., Araujo R., Huizar L., Rowley D., Buehler E., Dunn P., Gonzalez A., Kremetskaia I., Kim C., Lenz C., Li J., Liu S., Lueros S., Schwartz J., Shinn P., Toriumi M., Vystotskaya V.S., Walker M., Yu G., Ecker J., Theologis A., Davis R.W.; |
| RA | Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases. |
| CC | -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES. |
| DR | EMBL; AC007504; AAD43169.1; -; |
| DR | HSSP; PI2931; IRMK. |
| DR | InterPro; IPR000719; Euk.pkinase. |
| DR | InterPro; IPR002965; P-rich.extensn. |
| DR | InterPro; IPR002290; Ser.thr.pkinase. |
| DR | InterPro; IPR004040; STY.pkinase. |
| DR | Pfam; PF00069; pkinase; 1. |
| DR | PRINTS; PR01217; PRICHEXTENS. |
| DR | ProDom; |

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| DR | PROLINE; PS00011; PROTEIN_KINASE_DOM; 1. |
| DR | PROSITE; PS00108; FRCTIN_KINASE_ST; 1. |
| KW | ATP-binding; Hypothetical protein; Transferase. |
| SQ | SEQUENCE 710 AA; 75371 MW; 8B4420A8DD8F3AA6 CRC64; |

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|-----------------------|------------------|--------------------|-------------|-------------|
| Query Match: | 43.98; | Score 1515.5; | DB 10; | Length 710; |
| Best Local Similarity | 46.28; | Pred. No. 3.6e-90; | | |
| Matches 333; | Conservative 81; | Mismatches 156; | Indels 149; | Gaps 19; |

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|----|-----|---|
| QY | 2 | SSASP-SGTGSPSPSPNSITUTPPPA-----SAPPTTPSSPPSTI 44 |
| Db | 27 | SAAPPDTSAPPSPADS---SEPPALPSLPAVTFSPPTVSFPPIIDSSPPPD 83 |
| QY | 45 | PTSGPPSRGTRTSPAPP-----SPPTP-----STPCSP 72 |
| Db | 84 | --TPPSSPPDPADPPPIPIVFPPPIDSPPESTNSPPPEVEFPPPPADADESPAPP 141 |
| QY | 73 | PP--LPQ-----SPAPTPG-SPEAPVTPTRN-----PPSV 104 |
| Db | 142 | PPEGLPASPSGGPKKKHHPGATSPASAPATSPAPNAPPRNSSHALPKST 202 |
| QY | 105 | P--GPSPNPREGSPRPSPSPSPSSDGLSTGVVGIALGGVALIVTLICLCK 162 |
| Db | 202 | AAGPLTSPR--GYPSSGSNVPPANSNGGYQGKTWAGFAIAGFAVIALMAVVFLVRK 259 |
| QY | 163 | KRRDE--EAYIVPPP-----PPPGKAGGYGGQQOOWRQONATPPSDH 206 |
| Db | 260 | KKRIDAYSQYLPPSNFISIKSDGLYGQNTKGYSGPGYNQQQS--NSGN 312 |
| QY | 207 | VTVSLPPPKASPSPROP PPPPPMSGGSDYSDRVLPVPSPGLVLGFSKSTTYE 265 |
| Db | 313 | -----FGSQGGGGYTRSGSAPOSA---VMGSGOTHTYE 344 |
| QY | 267 | ELARATNGFEANLLGGGFGYVHKGLPSGKEVAVKOLKVGSOGREFOAEVILSRV 326 |
| Db | 345 | ELDTIEGFSKHNLIGEGFGCYKGKINDGKLAVAKOLKVGSOGDREFKAEEVILSRV 404 |
| QY | 327 | HHRHLVSLGYCZAGAKRLIVBFVPPNNLEHLHGGRPTMESTWRKLALGSAKLSY 386 |
| Db | 405 | HHRHLVSLGYCIADSERLLIYEVYPNOTLEHLHGKGRPVLEWARVRVIAIGSAKGLAY 464 |
| QY | 387 | LHEDCNPKLIHRDIKASNILLDFEFAKYADFGLAKTASTNTHVSTRVAGTGYLEPY 446 |
| Db | 465 | LHEDCHPKLIHRDIKASNILLDFEFAQAQADFGLAKLNDSTQTHTVSTRVAGTGYLEPY 524 |
| QY | 447 | AASGKLTESDVFSFGVILELITGRPRVDANNVYDDSLVDMARPLLNRASOGDPEGL 506 |
| Db | 525 | AQSGKLTDSVFSFGVILELITGRKPVOYOPLGESLVEMARPLLHKAITGDSEL 584 |
| QY | 507 | ADAKMNQDYDEMARMVACAAVCRHSAARRPRPMQIVRALBNQVSLSDLNENGRMPGS 566 |
| Db | 585 | VDRLEKHYVENEFVFMETAAACVRHSQPKPRMVQVVVRALDSEGDMGDISNGNKVQS 644 |
| QY | 567 | NVTSSYGGSTDYDSSCYNEDMKFRKMLGTQYNATGEYSNTSYDGLYPSGSSSEGQT 626 |
| Db | 645 | SA-----YDSGGYNNDTMFKRMAFSFDDSSDSGMYS---GDYSVODSRKSGNGAS 692 |
| QY | 627 | T 627 |
| Db | 693 | S 693 |

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| RESULT 11 | |
| Q9LV50 | PRELIMINARY; PRT; 567 AA. |
| ID | |
| Q9LV50 | |
| AC | |
| DT | 03-OCT-2000 (TrEMBLrel. 15, Created) |
| DT | 01-OCT-2000 (TrEMBLrel. 15, Last sequence update) |
| DT | 01-MAR-2002 (TrEMBLrel. 20, Last annotation update) |
| DE | Protein kinase-like protein. |
| OS | Arabidopsis thaliana (Mouse-ear cress). |
| OC | Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; |
| OC | Spermatophyta; Magnoliopsida; eudicotyledons; core eudicots; Rosidae; |

euroids II; Brassicales; Brassicaceae; Arabidopsis.
NCBI_TaxID=3702;
[1]
RN SEQUENCE FROM N.A.
RC STRAIN-COLUMBIA:
RA Kaneko T., Kato T., Sato S., Nakamura Y., Asamizu E., Tabata S.;
RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
[2]
RN SEQUENCE FROM N.A.
RC STRAIN-COLUMBIA:
RX MEDLINE-20363099; PubMed-10907853;
RA Nakamura Y.;
RI "Structural analysis of Arabidopsis thaliana chromosome 3. II.
Rt Sequence features of the regions of 4,251,695 bp covered by ninety PL,
RT TAC and BAC clones.";
RL DNA RES. 7:217-221(2000).
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL; AB020746; BAB02005.1; -.
DR InterPro: IPR000719; Euk.pkinase.
DR InterPro: IPR002290; Ser_thr.pkinase.
DR InterPro: IPR004040; sty.pkinase.
DR Pfam: PF00069; pkinase; 1.
DR ProDom: PD000001; Euk.pkinase; 1.
DR SMART: SM00221; STYK; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_AIP; 1.
DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 567 AA; 63160 MW; EC85F6DE26855387 CRC64;

Query Match 43.8%; Score 1513.5; DB 10; Length 567;
Best Local Similarity 64.9%; Pred. No. 3.5e-90;
Matches 311; Conservative 31; Mismatches 38; Indels 93; Gaps 7;

QY 98 RNPPSPVGPSPNPSRSGSGSRPPS-----SPSPSPSSDGLSTGVTVGTAIGSVALLVI 152
DB 177 RNPP-----PPASPS--GQEPPTMTPTPGFSLSPSPSR--LSTSAVVGISIGGG--VFV 225
QY 153 VTLCILCAKKRRDEDAIVYPPPPPKAGGPGYGGQQQRQQAATPPSDHVVTSLP 212
DB 226 LTLFFCKKKRPRDK-----ALP 245
QY 213 PPKAPSPRPQPPPPPPPPMSGGSDYSDRPVLPPLPPSPGLVLGFSKSTFTYEELARAT 272
DB 246 AP-----IGLVLIHQSTFTYGLARAI 268
QY 273 NPTSEANMLQGGFGYVHKGLPSGKTAVAKQLKVGSGQGEREQARVEIISRVHRLV 332
DB 269 NKTSEANMLGEGFGFYKGLANGNEVAVKQLKVGSAQGEKFEQAEVNTISQIHRRNL 328
QY 333 SLVGYCTAGAKRLVLYEFVFNNNLELHLHCEGRPTMEWSTRKLALGSAKGLSVLHEDCN 392
DB 329 SLVGYCTAGAORLLVYEFVFNNTLEFHLHCKGRPTMEWSRLKIAVSSSKGLSYLHENCN 368
QY 393 PKTIHRDIKASNLILDFKFEAKYADFGLAKIASDNTHTVSTRVMTGTFGLAPYAAAGKL 452
DB 389 PKTIHRDIKAANILIDFKFEAKYADFGLAKIALDNTHTVSTRVMTGTFGLAPYAAAGKL 448
QY 453 TEKSDVSEGVWLELITGRPRVDANNVYDSDLVDPWARPDLNRASEOGDFEGLADAKMN 512
DB 449 TEKSDVSYSGVWLELITGRPRVDANNVYADSDLVDPWARPDLVQALESFGLADIKLN 508
QY 513 NGVDREMARVACAACVRRHSARRPRMSQIVRALEGNVSLSDLENGMRPGQSNWYSS 571
DB 509 NEVDREMARVACAACVRYTHARRPRMDQVVRVLEGNISPSDLAQGITPGHSNWYSS 567

RESULT 12
Q9SX31 PRELIMINARY; PRT; 708 AA.
AC Q9SX31;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)

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01-MAR-2002 (Tremblrel. 20, Last annotation update)
DE F24J5.8 protein (Hypothetical 75.1 kDa protein).
GN F24J5.8.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [21]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. COLUMBIA;
RA Vysotskaia V.S., Schwartz J.R., Yu G., Toriumi M., Lenz C., Liu S.,
RA Lee J.M., Li J., Gonzalez A., Liu A., Liu K., Vaysberg M., Sakano H.,
RA Chin C., Choi E., Chiou J., Altafi H., Araujo R., Brooks S.,
RA Buehler E., Chao Q., Conn L., Conway A.B., Dunn P., Hansen N.,
RA Hwang B., Huizar L., Khan S., Kim C., Palm C., Rowley D., Shinn P.,
RA Walker M., Davis R.W., Ecker J.R., Federspiel N.A., Theologis A.,
RT *The sequence of BAC F24J5 from Arabidopsis thaliana chromosome 1.;
RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
RN [21]
RP SEQUENCE FROM N.A.
RC STRAIN=COLUMBIA;
RA Yamada K., Liu S.X., Sakano H., Pham P.K., Banh J., Chung M.K.,
RA Goldsmith A.J., Lee J.M., Quach H.L., Tang C., Toriumi M., Yu G.,
RA Bowser L., Carninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J.,
RA Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Koesema E.,
RA Lam B., Lin J., Meyers M.C., Miranda M., Narusaka M., Nguyen M.,
RA Palm C.J., Sakurai T., Satou M., Seki M., Shinn P., Southwick A.,
RA Shinozaki K., Davis R.W., Ecker J.R., Theologis A.,
RT *Full length cDNA of gene F24J5.8 (GI:5734709).;
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL; AC008075; AAD49974.1; -
DR EMBL; AY035076; AAK59581.1; -
DR InterPro; IPR000719; Euk_kinase.
DR InterPro; IPR002965; P-rich_extensions.
DR InterPro; IPR004290; Ser_thr_kinase.
DR Pfam; PF00069; pkinase; 1.
DR PRINTS; PR01217; PRICHEXTNSN.
DR ProDom; PD000001; Euk_kinase; 1.
DR SMART; SM00221; STKC; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Hypothetical protein; Serine/threonine-protein kinase;
KW Transferase.
SQ SEQUENCE 708 AA; 75127 MW; AC0818E54B076328 CRC64;

Query Match 42.3%; Score 1459.5; DB 10; Length 708;
Best Local Similarity 41.8%; Pred. No. 1.5e-86;
Matches 317; Conservative 90; Mismatches 127; Indels 225; Gaps 21;

QY 1 MSSAP-----SPGCGSPSPSPNSST-TTPPPASAP-PTTTP---SSPPPTTPTSP 48
DQ 1 MATIPVQPPVSNPPVTSPPLNNATSPATPPVTSPPLPPSPAPPNRPPTTPTSP 60
QY 49 PPSRSSTP-----SAPPSPPTTPTSPPLPQP-----SPP---ATTP 86
DQ 61 PVPANGAPPPLPKAPPSSSPFPQPVPISPPPTSPPTSPPTSPAPPALVPLP 120
QY 87 GSPAP--VTPP-----TRNPPPSV-----PQPSN--PREGGSPRPPSP-- 124
DQ 121 SSPPPASVPPPPSPPPILVRSPPSVRIQSPPTPPSDRPTQSPPPSPSPSPERP 180
QY 125 --SPPSPSSDGLSTGVVVGIAIGVALLVITLICLCCKKRRDEADYVPPPPPPG 182
DQ 181 TQSPSPSPS-----ERPTQSPSPSPSP-- 202
QY 183 KAGPGYGCQQQWQQNATPPSDHVTSILPAPK--APSPPTPPPPPPPPPPMS----- 234
DQ 203 -----SPPSDRPSQSPPPPPEDIKPPRPSNPPPTTFFSPRSP 244
QY 235 -----SSGGSDYSDRPLPPE----- 250

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|-----------|---|--|--------------|
| QY | 109 | SNPSREGGSPRPSPSPSPSP-----SDGLSTGVVVGIAAGWALLVTVL----CLL | 150 |
| Dd | 296 | SPPKSYSGVPMP-SPNPTPTDNTSSGSIAAVGVGSIG--VALVLLTILVVVVCC | 352 |
| QY | 160 | CKKKRRDEEDAYVYPPPPGRKAGGPYGQQQWRQOQTTPSDHVVTSLPPLPKAPS | 219 |
| Dd | 353 | KKKRKLSTGGGYVMTP-----MSSKSPRSDSAL--LKTOSAPL | 392 |
| QY | 220 | PPROPFPFPMSSSGSDSIDRPLPFPSPGLVLGFESKSTFTYEELARATNGFSEAN | 279 |
| Dd | 393 | V-----GNRSSNRITYLSQSEP-GFGQSRELFSYEELVIATNGFSDEN | 434 |
| QY | 280 | LLGGGFGFYHKGVLPSCKEVAVYAKLVKVSQGGEREFOAEVETISRVRHRHLVSLVGYCI | 339 |
| Dd | 435 | LLGEGFGFYKGVLPDERVAVYAKLVKLTGGQGDREFKAEDVTISRVRHRNLMSVGYCI | 494 |
| QY | 340 | AGAARLVYEPVNNLEHLHGFRPTMEWSTRKIALGSAKGLSYLHEDCNPKLIHRD | 399 |
| Dd | 495 | SENRLIUYDKVNNLYFHLLH--GTPELDWAIRVKIAAAGARGLAYLHEDCHPRIIHRD | 552 |
| QY | 400 | IKASNIILDFKEAKVADFGIAKIASTINTHVSRVMGTFFGLAPEYAASGKLTSEKSDVF | 459 |
| Dd | 553 | IKSSNILENNHALVSDFGLAKLALDONTHTITRYMCTFGYMAPEYASSGKLTSEKSDVF | 612 |
| QY | 460 | SPGVVLELITGRPVDANNVYDDSLVDNARPILNRASEOQDFGLADAKMNNGYDREE | 519 |
| Dd | 613 | SPGVVLELATITGRKVPDASPLGDESIVENARPTELSNATEETEETALADPKLRNVYGE | 672 |
| QY | 520 | MARMVCAACVRSARRPRMSOIIVALEGNVSLDLNEGMRCQSNVSYSGGSTDYD | 579 |
| Dd | 673 | MERMIEAAAACIRHSATKRPMISOIVRAF-D-SLAEEIDLTMGRIGSEI-----IN | 722 |
| QY | 580 | SSOVNEDMKFKRMALGTQYN 601 | |
| Dd | 723 | SAQQAERLFMRMFQSQNY 744 | |
| | | | |
| RESULT 15 | | | |
| Q9ZUEQ | | | |
| ID | Q3ZUE0 | PRELIMINARY; | PRU; 731 AA. |
| AC | Q3ZUE0 | | |
| DT | 01-MAY-1999 | (TREMBLrel. 10, Created) | |
| DT | 01-MAY-1999 | (TREMBLrel. 10, Last sequence update) | |
| DT | 01-XAR-2002 | (TREMBLrel. 20, Last annotation update) | |
| DE | F508.10 | protein. | |
| GN | NCBI_Taxid=3702; | | |
| OS | Arabisopsis thaliana (Mouse-ear cress). | | |
| OC | Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; | | |
| OC | Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; | | |
| OX | eurosid II; Brassicales; Brassicaceae; Arabidopsids. | | |
| RN | [1] | | |
| RP | SEQUENCE FROM N.A. | | |
| RC | STRAIN=CV. COLUMBIA; | | |
| RA | Vysotskaia V.S., Schwartz J.R., Yu G., Toriumi M., Liu S., Lenz C., | | |
| RA | Li J., Kremenetskaia I., Iurou J., Altafi H., Gonzalez A., Araujo R., | | |
| RA | Buehler E., Conn L., Conway A.B., Dunn P., Hansen N., Huizar L., | | |
| RA | Kim C., Palm C.J., Rowley D., Shinn P., Walker M., Davis R.W., | | |
| RA | Ecker J.R., Federspiel N.A., Theologis A.; | | |
| RT | "Arabidopsis thaliana chromosome I BAC F508 sequence."; | | |
| RL | Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases. | | |
| RN | [2] | | |
| RP | SEQUENCE FROM N.A. | | |
| RC | STRAIN=CV. COLUMBIA; | | |
| RA | Theologis A.; | | |
| RL | Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases. | | |
| CC | -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES. | | |
| DR | EMBL; AC005990; AAC98010.1; - | | |
| DR | InterPro; IPRO00719; Euk.pkinase. | | |
| DR | InterPro; IPRO02965; Ser_thr_pkinase. | | |
| DR | InterPro; IPRO02290; Per_thr_pkinase. | | |
| DR | Pfam; PF00069; pkinase.i. | | |
| DR | PRINTS; PR01217; PRICHEXTENS. | | |

| | | |
|----|--|--|
| DR | ProDom: PD000001; Euk_pkinase: 1. | |
| DR | PROSITE; PS00107; PROTEIN_KINASE_ATP; 1. | |
| DR | PROSITE; PS00107; PROTEIN_KINASE_DOM; 1. | |
| DR | PROSITE; PS00108; PROTEIN_KINASE_ST; 1. | |
| DR | ATP-binding; Serine/threonine-protein kinase; Transferase. | |
| SO | SEQUENCE 731 AA; 77639 MW; 45D9AD5C450001B CRC64; | |

| | | |
|-----------------------|--|--|
| Query Match | | 41.0%; Score 1415.5; DB 10; Length 731; |
| Best Local Similarity | | 43.4%; Pred. No. 1.1e-83; |
| Matches | | 321; Conservative 93; Mismatches 156; Indels 169; Gaps 22; |

| | | | | |
|----|-----|---|-----------------------------------|-----|
| QY | 2 | SSAPSPGTSPPSPSPSNSTTT-----TTPPAS----- | -----APPTPTSPSPPP | 40 |
| | | : ::: | : : | |
| Db | 29 | NSALPPVDSPPSPADSSSTPLSEPTTPPSQLPLPLSPILPTFLSPPPSPDSSPPV | 88 | |
| QY | 41 | PSIHTGPPSPSSSTPSAP-----PPSPPTSPGSPPP-----LQPSPPA-----PTTP | 86 | |
| | | : : : : : : | : : : : | |
| Db | 89 | DST-PSPPPTSNESPSPPEDSETTPAPPNESNDNPPSQDIQSPSPSPSNVGTNP | 147 | |
| QY | 87 | GSPP--APVTPTKNP---PPSVGGPPSPN---SREGGSRPPSPSP--SPSPS | ----- | 129 |
| | | : : : : : : : | : : : : | |
| Db | 148 | ESPPLOSPPAPEASDPTNSPPASPLDTPPIQPSGPAISPANPNAPSPPTVPKKT | 207 | |
| QY | 130 | -----SSDGLSTG----- | -----VTVG:AIGVALLVITLICLL | 159 |
| | | : : : : : : : | : : : : : | |
| Db | 208 | PSSGPVVSPLTSPSKGTPTPNOGDDGGGGGYQKTNVGHAVAGFAMALIGVFLV | 267 | |
| QY | 160 | CKKKRRDEDAY-----YVPPP----- | -----PPGPKAGGPGYGGGQOQQOQQNATP | 202 |
| | | : : : : : : : | : : : : : | |
| Db | 268 | RKKKKR--NIDSYNHSOYLDPHPNFSVKSDGLYQDPGKGYSQSPNGSMYNNQQOQSSM | 325 | |
| QY | 203 | PSDHVTVSLPPKAPSPPPQPPPPPPSPMSSGGSDYSDRVLPPSPGLVGLGSKST | 262 | |
| | | : : : : : : : | : : : : : | |
| Db | 326 | GNYSYTAG-----GGVPHHQ----- | -----MQSSGTPD----- | 358 |
| QY | 263 | FTYEELARATNGFSEAKLQGGGFGYVHKVLPSGKEVAVKQLKVGSGGGEREQFAVEI | 322 | |
| | | : : : : : : : | : : : : : : | |
| Db | 339 | FSYEELAEITQGFARKNILGEGGCVYKCTLQDGKVVAVKQLKAGSGDGRFKAIVEI | 418 | |
| QY | 323 | ISRVHHRHLYSLGYCIAGAKRLWTVEYVNNMLELHLHGEGRPTMEWSTRLKIALGSAK | 382 | |
| | | : : : : : : : | : : : : : | |
| Db | 419 | ISRVHHRHLYSLGYCISDQERLLIYVSNQTLLEHLH-----EWSKRVRIALGSAK | 471 | |
| QY | 383 | GLSVLHEDCNPKIITHRIDIKASNTILDFKPEAK----- | -----VADFGIAKIA | 424 |
| | | : : : : : : | : : : : | |
| Db | 472 | GLAELEHDCPKIITHRIDIKASNTILDEEQAQIMKSSSELNLSYCKVLVADFGIARLN | 531 | |
| QY | 425 | SOINTHVSRVMGTFCYLAPEYAAASKLIEKSDVFSFGVVLLELITGRFPVDANNVYVD | 484 | |
| | | : : : : : : : | : : : : | |
| Db | 532 | DTTQTHVSRVMGTFCYLAPEYASSGKLITDRSDVFSFGVVLLELTVGTRKPDQTQPLGE | 591 | |
| QY | 485 | SLVNDWAPRLNRASEGDFEGLADAKMNNGYDEEVARVACAAACVRHSARBRPMSQI | 544 | |
| | | : : : : : : : | : : : : | |
| Db | 592 | SLVEMARPLLKAEITGDSLECLDTLEKRYVEHFVRIETAAACVRSGPKRPKRVQV | 651 | |
| QY | 545 | VRALEGNVSLDNLGMRPESQSNVSYSGGSDYDSSQYNEDMKFKKALGTQETNATG | 604 | |
| | | : : : : : : : | : : : : | |
| Db | 652 | VRALDCDGGSDISNGIKIGQ----- | -----STITYDSQYNEDIMKFKAMFGDGNWESS | 702 |
| QY | 605 | EYSNPTSDYGLYPSGSSSE | 623 | |
| | | : : : : : : : | : : : : : | |
| Db | 703 | LXS-----GNYSAKSSSD | 715 | |